

# V

## HIV-1/SIVcpz Proteins

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### V-1 Introduction

The HIV-1/SIVcpz protein alignments are based on the complete genome nucleotide alignment, but in some cases a few sequences were removed because they were too short to be informative (especially in Nef), had many stop codons or a problematic segment of amino acids. As with the other alignments in this compendium, they are intended to display the genetic variation of the world-wide HIV epidemic in a compact form. They are annotated in more detail than the complete genome nucleotide alignment.

## V-2 Annotated features

Features of HIV-1 annotated in the alignment that follows.

Feature	Protein	Location	Page
Gag start, p17 start	Gag	1	324
membrane binding	Gag	1-30	324
phosphorylation site	Gag	112	324
p17 end	Gag	132	326
p24 start	Gag	133	326
CyPA binding	Gag	205-241	326
major homology region	Gag	285-304	326
p24 end	Gag	364	328
p2 start	Gag	365	328
p2 end	Gag	377	328
p7 start	Gag	378	328
Zn motif	Gag	392-404	328
Zn motif	Gag	413-425	328
p7 end	Gag	432	328
p1 start	Gag	433	328
p1 end	Gag	448	330
p6 start	Gag	449	330
Vpr binding	Gag	455-460	330
Vpr binding	Gag	489-494	330
p6 end, Gag end	Gag	501	330
Pol start	Pol	1	332
Gag-Pol TF start	Pol	1	332
Gag-Pol TF end	Pol	56	332
protease start	Pol	57	332
protease end	Pol	155	334
p66, p51 RT start	Pol	156	334
M41L	Pol	196	334
D67N	Pol	222	334
K70R	Pol	225	334
D110 catalytic site	Pol	265	334
polymerase motif	Pol	337-342	336
M184V	Pol	339	336
T215Y	Pol	370	336
K219Q	Pol	374	336
p51 RT end	Pol	595	338
p15 RNase H start	Pol	596	338
p66 RT, p15 Rnase H end	Pol	715	340
p31 Integrase start	Pol	716	340
p31 Integrase end	Pol	1004	344
Pol end	Pol	1004	344
Vif start	Vif	1	346
Vif end	Vif	193	348
Vpr start	Vpr	1	350
oligomerization	Vpr	1-41	350
amphipathic $\alpha$ -helix	Vpr	17-33	350
H(S/N)RIG motifs	Vpr	71-83	350
frameshift in HXB2	Vpr	72	350
Vpr end in HXB2	Vpr	79	350

Feature	Protein	Location	Page
Vpr end	Vpr	98	350
Tat start	Tat	1	352
C-rich region	Tat	22-37	352
nuclear localization	Tat	49-57	352
exon 1 end	Tat	72	352
exon 2 start	Tat	73	352
Tat end	Tat	102	352
Rev start	Rev	1	354
exon 1 end	Rev	25	354
exon 2 start	Rev	26	354
NLS	Rev	34-49	354
Leu-rich effector domain	Rev	75-83	354
Rev end	Rev	117	354
Vpu start	Vpu	1	356
transmembrane domain	Vpu	1-27	356
cytoplasmic domain	Vpu	28-82	356
$\alpha$ -helix	Vpu	43-51	356
phos	Vpu	53	356
phos	Vpu	57	356
$\alpha$ -helix	Vpu	58-70	356
Vpu end	Vpu	83	356
Env start	Env	1	358
signal peptide end	Env	30	358
gp120 start	Env	31	358
glycosylation NVT	Env	88-90	358
CD4 binding	Env	124	358
V1	Env	131-156	358
glycosylation NDT	Env	136-138	358
glycosylation NSS	Env	141-143	360
glycosylation NCS	Env	156-158	360
V2	Env	158-196	360
glycosylation NIS	Env	160-162	360
glycosylation NDT	Env	186-188	360
glycosylation NTS	Env	197-199	360
CD4 binding	Env	196	360
glycosylation NKT	Env	230-232	360
glycosylation NGT	Env	234-236	360
glycosylation NVS	Env	241-243	360
glycosylation NGS	Env	262-264	362
glycosylation NFT	Env	276-278	362
CD4 binding	Env	279	362
glycosylation NTS	Env	289-291	362
glycosylation NCT	Env	295-297	362
V3	Env	296-331	362
glycosylation NNT	Env	301-303	362
V3 tip	Env	312-315	362
glycosylation NNT	Env	339-341	362
glycosylation NKT	Env	356-358	362
CD4 binding	Env	365	362
V4	Env	385-418	364
glycosylation NST	Env	386-388	364
glycosylation NST	Env	392-394	364
glycosylation NST	Env	397-399	364

Feature	Protein	Location	Page
glycosylation NNT	Env	406-408	364
CD4 binding	Env	425	364
glycosylation NIT	Env	448-450	364
CD4 binding	Env	455	364
V5	Env	460-471	364
glycosylation NES	Env	463-465	364
CD4 binding	Env	469	364
fusion peptide	Env	512-527	364
gp120 end	Env	511	364
gp41 start	Env	512	364
immunodominant region	Env	588-607	366
glycosylation NAS	Env	611-613	366
glycosylation NKS	Env	616-618	366
glycosylation NHT	Env	624-626	366
glycosylation NYT	Env	637-639	366
transmembrane domain	Env	685-704	368
gp41 cytoplasmic tail start	Env	705	368
glycosylation NGS	Env	750-752	368
glycosylation NAT	Env	816-818	368
cytoplasmic tail end	Env	857	370
gp41 end	Env	857	370
Env end	Env	857	370
Nef start	Nef	1	372
myristoylation	Nef	2-7	372
acidic cluster	Nef	62-65	372
poly-P helix	Nef	69-78	372
phosphorylation	Nef	77-81	372
HXB2 premature Nef end	Nef	124	374
normal Nef end	Nef	207	374

### V-3 Sequences

Sequences included in the HIV-1 protein alignments.

Name	Accession	Proteins	Author	Reference
B.FR.83.HXB2	K03455	All	Wong-Staal, F.	<i>Nature</i> <b>313</b> (6000):277-284 (1985)
A1.CM.08.886_24	KP718928	All	Luk, K.-C.	<i>PLoS One</i> <b>10</b> (11); e0141723 (2015)
A1.CY.08.CY236	JF683783	All	Kousiappa, I.	<i>ARHR</i> <b>27</b> (11); 1183-99 (2011)
A1.KE.11.DEMA111KE002	KF716474	All	Sanchez, A.M.	<i>J Immunol Methods</i> <b>2014</b> Jul;409:117-30 doi: 101016/jjim201401004 Epub 2014 Jan 19
A1.NG.10.10NG040248	KX389608	All	Heipertz, R.A. Jr.	<i>Medicine(Baltimore)</i> <b>95</b> (32):E4346 (2016)
A1.PK.14.DEMA114PK001	KU749409	All	Hora, B.	Unpublished
A1.RW.11.DEMA111RW002	KF716472	All	Sanchez, A.M.	<i>J Immunol Methods</i> <b>2014</b> Jul;409:117-30 doi: 101016/jjim201401004 Epub 2014 Jan 19

Name	Accession	Proteins	Author	Reference
A1.UG.11.DEMA110UG009	KF716486	All	Sanchez, A.M.	<i>J Immunol Methods</i> <b>2014</b> Jul;409:117-30 doi: 101016/jjim201401004 Epub 2014 Jan 19
A1.ZA.04.503_15344_T10_A1	KT183312	All	Hertz, T.	<i>Vaccine</i> <b>34</b> (47); 5792-5801 (2016)
A2.CM.01.01CM_1445MV	GU201516	All	Carr, J.K.	<i>Retrovirology</i> <b>2010</b> Apr 28;7:39 doi: 101186/1742-4690-7-39
A3.SN.01.DDI579	AY521629	All	Meloni, S.T.	<i>J Virol</i> <b>78</b> (22):12438-12445 (2004)
A4.CD.97.97CD_KCC2	AM000053	All	Vidal, N.	<i>ARHR</i> <b>22</b> (2):182-187 (2006)
A6.BY.13.PV85	KT983615	All	Sasinovich, S.	Unpublished
A6.CY.09.CY255	JF683798	All	Kousiappa, I.	<i>ARHR</i> <b>27</b> (11); 1183-99 (2011)
A6.RU.11.11RU6950	JX500694	All	Baryshev, P.B.	<i>ARHR</i> <b>30</b> (6); 592-7 (2014)
A6.UA.12.DEMA112UA014	KU749402	All	Hora, B.	Unpublished
B.BR.10.10BR_RJ032	KJ849801	All	Pessoa, R.	<i>Transfusion</i> <b>55</b> (5); 980-90 (2015)
B.CA.07.502_1191_03	JF320424	All	Rolland, M.	<i>Nat Med</i> <b>17</b> (3); 366-71 (2011)
B.CH.08.M2_0803101_NFLG8	KC797225	All	Castro, E.	<i>AIDS</i> <b>28</b> (12); 1840-4 (2014)
B.CN.12.DEMB12CN006	KP109511	All	Hora, B.	Unpublished
B.CU.14.14CU005	KR914676	All	Blanco, M.	Unpublished
B.DE.13.366396	KT124767	All	Tully, D.C.	<i>PLoS Pathog</i> <b>12</b> (5); e1005619 (2016)
B.ES.14.ARP1195	KT276255	All	Cuevas, M.T.	Unpublished
B.FR.11.DEMB11FR001	KF716496	All	Sanchez, A.M.	<i>J Immunol Methods</i> <b>2014</b> Jul;409:117-30 doi: 101016/jjim201401004 Epub 2014 Jan 19
B.HT.05.05HT_129389	EU839602	All	Nadai, Y.	<i>PLoS ONE</i> <b>4</b> (3):E4814 (2009)
B.JP.12.DEMB12JP001	KF716498	All	Sanchez, A.M.	<i>J Immunol Methods</i> <b>2014</b> Jul;409:117-30 doi: 101016/jjim201401004 Epub 2014 Jan 19
B.KR.07.HP_18_07JHS10_3909	KJ140263	All	Kim, B.-R.	<i>Haemophilia</i> <b>21</b> (1); e1-11 (2015)
B.RU.11.11RU21n	JX500708	All	Baryshev, P.B.	Unpublished
B.SE.12.SE600057	KP411828	All	Grossmann, S.	<i>J Int AIDS Soc</i> <b>2015</b> Jun 25;18:20035 doi: 107448/IAS18120035 eCollection 2015
B.TH.10.DEMB10TH002	KP109514	All	Hora, B.	Unpublished
B.US.16.2609	KX505536	All	Bruner, K.M.	<i>Nat Med</i> <b>22</b> (9); 1043-9 (2016)
C.BR.11.DEMC11BR035	KU749393	All	Hora, B.	Unpublished
C.CN.10.YNFL19	KC870038	All	Wei, H.	Unpublished
C.DE.10.622166	KT124786	All	Tully, D.C.	<i>PLoS Pathog</i> <b>12</b> (5); e1005619 (2016)
C.ES.14.ARP1198	KT276258	All	Cuevas, M.T.	Unpublished
C.ET.08.ET104	KU319528	All	Amogne, W.	<i>ARHR</i> <b>32</b> (5); 471-4 (2016)
C.IN.15.NIRT008	KX069226	All	Aralaguppe, S.G.	<i>J Virol Methods</i> <b>2016</b> Oct;236:98-104 doi: 101016/jjviromet201607010 Epub 2016 Jul 19
C.MW.09.703010256_CH256.w96	KC156214	All	Parrish, N.F.	<i>PNAS USA</i> <b>110</b> (17); 6626-33 (2013)
C.NG.10.10NG020523	KX389612	All	Heipertz, R.A. Jr.	<i>Medicine(Baltimore)</i> <b>95</b> (32):E4346 (2016)

Name	Accession	Proteins	Author	Reference
C.NP.11.11NP016	KU341724	All	Bhusal, N.	<i>Curr HIV Res</i> <b>14</b> (6):517-524 (2016)
C.PK.14.DEMC14PK009	KU749412	All	Hora, B.	Unpublished
C.SE.13.SE600311	KP411835	All	Grossmann, S.	<i>J Int AIDS Soc</i> <b>2015</b> Jun 25;18:20035 doi: 107448/IAS18120035 eCollection 2015
C.TZ.08.707010457_CH457.w8	KC156220	All	Parrish, N.F.	<i>PNAS USA</i> <b>110</b> (17); 6626-33 (2013)
C.US.11.17TB4_4G8	KF526226	All	Ho, Y.-C.	<i>Cell</i> <b>155</b> (3); 540-51 (2013)
C.ZA.13.DEMC13ZA152	KU749417	All	Hora, B.	Unpublished
C.ZM.11.DEMC11ZM006	KF716467	All	Sanchez, A.M.	<i>J Immunol Methods</i> <b>2014</b> Jul;409:117-30 doi: 101016/jjim201401004 Epub 2014 Jan 19
D.BR.10.10BR_RJ108	KJ787683	All	Pessoa, R.	<i>Genome Announc</i> <b>2</b> (3):e00586-14 (2014)
D.CD.03.LA17MuBo	KU168271	All	Berg, M.G.	<i>J Clin Microbiol</i> <b>54</b> (4); 868-82 (2016)
D.CM.10.DEMD10CM009	JX140670	All	Sanchez, A.M.	<i>J Immunol Methods</i> <b>2014</b> Jul;409:117-30 doi: 101016/jjim201401004 Epub 2014 Jan 19
D.CY.06.CY163	FJ388945	All	Kousiappa, I.	<i>ARHR</i> <b>25</b> (8); 727-40 (2009)
D.KE.11.DEMD11KE003	KF716476	All	Sanchez, A.M.	<i>J Immunol Methods</i> <b>2014</b> Jul;409:117-30 doi: 101016/jjim201401004 Epub 2014 Jan 19
D.KR.04.04KBH8	DQ054367	All	Cho, Y.-K.	<i>ARHR</i> <b>29</b> (4); 738-43 (2013)
D.TZ.01.A280	AY253311	All	Arroyo, M.A.	<i>ARHR</i> <b>20</b> (8):895-901 (2004)
D.UG.10.DEMD10UG004	KF716479	All	Sanchez, A.M.	<i>J Immunol Methods</i> <b>2014</b> Jul;409:117-30 doi: 101016/jjim201401004 Epub 2014 Jan 19
D.UG.11.DEMD11UG003	KF716480	All	Sanchez, A.M.	<i>J Immunol Methods</i> <b>2014</b> Jul;409:117-30 doi: 101016/jjim201401004 Epub 2014 Jan 19
D.YE.02.02YE516	AY795907	All	Saad, M.D.	<i>ARHR</i> <b>21</b> (7):644-648 (2005)
F1.AO.06.AO_06_ANG32	FJ900266	All	Guimaraes, M.L.	<i>Retrovirology</i> <b>6</b> , 39 (2009)
F1.AR.02.ARE933	DQ189088	All	Aulicino, P.C.	<i>ARHR</i> <b>21</b> (2):158-164 (2005)
F1.BR.10.10BR_RJ015	KJ849791	All	Pessoa, R.	<i>Transfusion</i> <b>55</b> (5); 980-90 (2015)
F1.BR.11.DEMF111BR037	KU749396	All	Hora, B.	Unpublished
F1.CY.08.CY222	JF683771	All	Kousiappa, I.	<i>ARHR</i> <b>27</b> (11); 1183-99 (2011)
F1.ES.02.ES_X845_4	FJ670516	All	Fernandez-Garcia, A.	<i>ARHR</i> <b>25</b> (11):1187-1191 (2009)
F1.ES.11.VA0053_nfl	KJ883138	All	Delgado, E.	<i>PLoS ONE</i> <b>10</b> (11):E0143325 (2015)
F1.FR.04.LA22LeRe	KU168276	All	Berg, M.G.	<i>J Clin Microbiol</i> <b>54</b> (4); 868-82 (2016)
F1.RO.03.LA20DuCl	KU168274	All	Berg, M.G.	<i>J Clin Microbiol</i> <b>54</b> (4); 868-82 (2016)

Name	Accession	Proteins	Author	Reference
F1.RU.08.D88_845	GQ290462	All	Fernandez-Garcia, A.	<i>ARHR</i> <b>25</b> (11):1187-1191 (2009)
F2.CM.02.02CM_0016BBY	AY371158	All	Kijak, G.H.	<i>ARHR</i> <b>20</b> (5):521-530 (2004)
F2.CM.10.DEMF210CM007	JX140673	All	Sanchez, A.M.	<i>J Immunol Methods</i> <b>2014</b> Jul;409:117-30 doi: 101016/jjim201401004 Epub 2014 Jan 19
F2.CM.11.DEURF11CM026	KU749422	All	Hora, B.	Unpublished
G.CD.03.LA23LiEd	KU168277	All	Berg, M.G.	<i>J Clin Microbiol</i> <b>54</b> (4); 868-82 (2016)
G.CM.08.789_10	KP718925	All	Luk, K.-C.	<i>PLoS One</i> <b>10</b> (11); e0141723 (2015)
G.CM.10.DEMG10CM008	JX140676	All	Sanchez, A.M.	<i>J Immunol Methods</i> <b>2014</b> Jul;409:117-30 doi: 101016/jjim201401004 Epub 2014 Jan 19
G.CM.10.DEURF10CM020	KP109502	All	Hora, B.	Unpublished
G.CN.08.GX_2084_08	JN106043	All	Liu, W.	<i>Zhonghua Liu Xing Bing Xue Za Zhi</i> <b>34</b> (1); 53-6 (2013)
G.ES.14.ARP1201	KT276261	All	Cuevas, M.T.	Unpublished
G.GH.03.03GH175G	AB287004	All	Takekawa, N.	Unpublished
G.GW.08.LA57LmNe	KU168300	All	Berg, M.G.	<i>J Clin Microbiol</i> <b>54</b> (4); 868-82 (2016)
G.KE.09.DEMG09KE001	KF716477	All	Sanchez, A.M.	<i>J Immunol Methods</i> <b>2014</b> Jul;409:117-30 doi: 101016/jjim201401004 Epub 2014 Jan 19
G.NG.12.12NG060409	KX389648	All	Heipertz, R.A. Jr.	<i>Medicine(Baltimore)</i> <b>95</b> (32):E4346 (2016)
H.CD.04.LA19KoSa	KU168273	All	Berg, M.G.	<i>J Clin Microbiol</i> <b>54</b> (4); 868-82 (2016)
H.CF.02.LA25LeMi	KU168279	All	Berg, M.G.	<i>J Clin Microbiol</i> <b>54</b> (4); 868-82 (2016)
H.GB.00.00GBAC4001	FJ711703	All	Holzmayr, V.	<i>ARHR</i> <b>25</b> (7):721-726 (2009)
J.CD.03.LA26DiAn	KU168280	All	Berg, M.G.	<i>J Clin Microbiol</i> <b>54</b> (4); 868-82 (2016)
J.CD.97.J_97DC_KTB147	EF614151	All	Abecasis, A.B.	<i>J Virol</i> <b>81</b> (16):8543-8551 (2007)
J.SE.93.SE9280_7887	AF082394	All	Laukkanen, T.	<i>ARHR</i> <b>15</b> (3):293-297 (1999)
K.CD.97.97ZR_EQTB11	AJ249235	All	Triques, K.	<i>ARHR</i> <b>16</b> (2):139-151 (2000)
K.CM.96.96CM_MP535	AJ249239	All	Triques, K.	<i>ARHR</i> <b>16</b> (2):139-151 (2000)
01_AE.AF.07.569M	GQ477441	All	Sanders-Buell, E.	<i>ARHR</i> <b>26</b> (5):605-608 (2010)
01_AE.CM.11.1156_26	KP718930	All	Luk, K.-C.	<i>PLoS One</i> <b>10</b> (11); e0141723 (2015)
01_AE.CN.12.DE00112CN011	KP109508	All	Hora, B.	Unpublished
01_AE.HK.04.HK001	DQ234790	All	Tsui, S.K.W.	Unpublished
01_AE.IR.10.10IR_THR48F	AB703616	All	Jahanbakhsh, F.	<i>ARHR</i> <b>29</b> (1); 198-203 (2013)
01_AE.JP.11.DE00111JP003	KF859741	All	Sanchez, A.M.	<i>J Immunol Methods</i> <b>2014</b> Jul;409:117-30 doi: 101016/jjim201401004 Epub 2014 Jan 19

Name	Accession	Proteins	Author	Reference
01_AE.SE.11.SE601018	KP411841	All	Grossmann, S.	<i>J Int AIDS Soc</i> <b>2015</b> Jun 25;18:20035 doi: 107448/IAS18120035 eCollection 2015
01_AE.TH.10.DE00110TH001	KP109513	All	Hora, B.	Unpublished
01_AE.TH.90.CM240	U54771	All	Carr, J.K.	<i>J Virol</i> <b>70</b> (9):5935-5943 (1996)
01_AE.US.05.306163_FL	JX863920	All	Heipertz, R.A. Jr.	<i>ARHR</i> <b>29</b> (10):1310-1320 (2013)
02_AG.CM.10.DE00210CM013	KF859739	All	Sanchez, A.M.	<i>J Immunol Methods</i> <b>2014</b> Jul;409:117-30 doi: 101016/jjim201401004 Epub 2014 Jan 19
02_AG.DE.09.701114	KT124792	All	Tully, D.C.	<i>PLoS Pathog</i> <b>12</b> (5); e1005619 (2016)
02_AG.GW.05.CC_0048	FJ694792	All	Vinner, L.	<i>APMIS</i> <b>119</b> (8); 487-97 (2011)
02_AG.KR.12.12MHI11_10746	KF561437	All	Cho, Y.-K.	Unpublished
02_AG.KR.12.12MHR9	KF561435	All	Cho, Y.-K.	Unpublished
02_AG.LR.x.POC44951	AB485636	All	Baesi, K.	<i>PLoS One</i> <b>9</b> (9); e105098 (2014)
02_AG.NG.12.12NG060418	KX389649	All	Heipertz, R.A. Jr.	<i>Medicine(Baltimore)</i> <b>95</b> (32):E4346 (2016)
02_AG.NG.x.IBNG	L39106	All	Howard, T.M.	<i>ARHR</i> <b>10</b> (12):1755-1757 (1994)
02_AG.SE.11.SE602024	KP411845	All	Grossmann, S.	<i>J Int AIDS Soc</i> <b>2015</b> Jun 25;18:20035 doi: 107448/IAS18120035 eCollection 2015
02_AG.SN.13.9580	KT223760	All	Aman, S.	Unpublished
03_AB.RU.97.KAL153_2	AF193276	All	Liitsola, K.	<i>ARHR</i> <b>16</b> (11):1047-1053 (2000)
04_cpx.CY.94.94CY032_3	AF049337	All	Gao, F.	<i>J Virol</i> <b>72</b> (12):10234-10241 (1998)
05_DF.BE.x.VI1310	AF193253	All	Laukkanen, T.	<i>Virology</i> <b>269</b> (1):95-104 (2000)
06_cpx.AU.96.BFP90	AF064699	All	Oelrichs, R.B.	<i>ARHR</i> <b>14</b> (16):1495-1500 (1998)
07_BC.CN.98.98CN009	AF286230	All	Rodenburg, C.M.	<i>ARHR</i> <b>17</b> (2):161-168 (2001)
08_BC.CN.97.97CNGX_6F	AY008715	All	Piyasirisilp, S.	<i>J Virol</i> <b>74</b> (23):11286-11295 (2000)
09_cpx.GH.96.96GH2911	AY093605	All	McCutchan, F.E.	<i>ARHR</i> <b>20</b> (8):819-826 (2004)
10_CD.TZ.96.96TZ_BF061	AF289548	All	Kouliniska, I.N.	<i>ARHR</i> <b>17</b> (5):423-431 (2001)
11_cpx.CM.95.95CM_1816	AF492624	All	Wilbe, K.	<i>ARHR</i> <b>18</b> (12):849-56 (2002)
12_BF.AR.99.ARMA159	AF385936	All	Carr, J.K.	<i>AIDS</i> <b>15</b> (15):F41-F47 (2001)
13_cpx.CM.96.96CM_1849	AF460972	All	Wilbe, K.	<i>ARHR</i> <b>18</b> (12):849-56 (2002)
14_BG.ES.05.X1870	FJ670522	All	Cuevas, M.T.	<i>ARHR</i> <b>26</b> (9); 1019-25 (2010)
15_01B.TH.99.99TH_MU2079	AF516184	All	Viputtijul, K.	<i>ARHR</i> <b>18</b> (16):1235-1237 (2002)
16_A2D.KR.97.97KR004	AF286239	All	Gao, F.	<i>ARHR</i> <b>17</b> (8):675-688 (2001)
17_BF.AR.99.ARMA038	AY037281	All	Carr, J.K.	<i>AIDS</i> <b>15</b> (15):F41-F47 (2001)
18_cpx.CU.99.CU76	AY586540	All	Thomson, M.M.	<i>AIDS</i> <b>19</b> (11):1155-63 (2005)
19_cpx.CU.99.CU7	AY894994	All	Casado, G.	<i>JAIDS</i> <b>40</b> (5):532-537 (2005)
20_BG.CU.99.Cu103	AY586545	All	Sierra, M.	<i>JAIDS</i> <b>45</b> (2):151-160 (2007)
21_A2D.KE.99.KER2003	AF457051	All	Dowling, W.E.	<i>AIDS</i> <b>16</b> (13):1809-1820 (2002)
22_01A1.CM.01.01CM_0001BBY	AY371159	All	Kijak, G.H.	<i>ARHR</i> <b>20</b> (5):521-530 (2004)
23_BG.CU.03.CB118	AY900571	All	Sierra, M.	<i>JAIDS</i> <b>45</b> (2):151-160 (2007)
24_BG.ES.08.X2456_2	FJ670526	All	Cuevas, M.T.	<i>ARHR</i> <b>26</b> (9); 1019-25 (2010)
25_cpx.CM.02.1918LE	AY371169	All	Kijak, G.H.	<i>ARHR</i> <b>20</b> (5):521-530 (2004)
26_AU.CD.02.02CD_MBTB047	FM877782	All	Vidal, N.	<i>ARHR</i> <b>25</b> (8):823-832 (2009)
27_cpx.FR.04.04CD_FR_KZS	AM851091	All	Vidal, N.	<i>ARHR</i> <b>24</b> (2):315-321 (2008)
28_BF.BR.99.BREPM12609	DQ085873	All	Sa Filho, D.J.	<i>ARHR</i> <b>22</b> (1):1-13 (2006)
29_BF.BR.01.BREPM16704	DQ085876	All	Sa Filho, D.J.	<i>ARHR</i> <b>22</b> (1):1-13 (2006)
31_BC.BR.04.04BR142	AY727527	All	Sanabani, S.	<i>ARHR</i> <b>22</b> (2):171-176 (2006)

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33_01B.ID.07.JKT189_C	AB547463	All	SahBandar, I.N.	<i>ARHR</i> <b>27</b> (1); 97-102 (2011)
34_01B.TH.99.OUR1969P	EF165539	All	Tovanabuttra, S.	<i>ARHR</i> <b>23</b> (6):829-833 (2007)
35_AD.AF.07.169H	GQ477446	All	Sanders-Buell, E.	<i>ARHR</i> <b>26</b> (5):605-608 (2010)
36_cpx.CM.00.00CMNYU830	EF087994	All	Powell, R.L.	<i>ARHR</i> <b>23</b> (8):1008-1019 (2007)
37_cpx.CM.00.00CMNYU926	EF116594	All	Powell, R.L.	<i>ARHR</i> <b>23</b> (7):923-933 (2007)
38_BF1.UY.03.UY03_3389	FJ213783	All	Ruchansky, D.	<i>ARHR</i> <b>25</b> (3); 351-6 (2009)
39_BF.BR.04.04BRRJ179	EU735535	All	Guimaraes, M.L.	<i>AIDS</i> <b>22</b> (3):433-435 (2008)
40_BF.BR.05.05BRRJ055	EU735537	All	Guimaraes, M.L.	<i>AIDS</i> <b>22</b> (3):433-435 (2008)
42_BF.LU.03.luBF_01_03	EU170151	All	Struck, D.	<i>ARHR</i> <b>31</b> (5); 554-8 (2015)
43_02G.SA.03.J11223	EU697904	All	Badreddine, S.	<i>ARHR</i> <b>23</b> (5):667-674 (2007)
44_BF.CL.00.CH80	FJ358521	All	Delgado, E.	<i>ARHR</i> <b>26</b> (7); 821-6 (2010)
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46_BF.BR.07.07BR_FPS625	HM026456	All	Sanabani, S.S.	<i>Virol J</i> <b>2010</b> Apr 16;7:74 doi: 101186/1743-422X-7-74
47_BF.ES.08.P1942	GQ372987	All	Fernandez-Garcia, A.	<i>ARHR</i> <b>26</b> (7); 827-32 (2010)
48_01B.MY.07.07MYKT021	GQ175883	All	Li, Y.	<i>JAIDS</i> <b>54</b> (2):129-136 (2010)
49_cpx.GM.03.N26677	HQ385479	All	de Silva, T.I.	<i>Retrovirology</i> <b>7</b> (1):82 (2010)
50_A1D.GB.10.12792	JN417240	All	Foster, G.M.	<i>PLoS One</i> <b>9</b> (1); e83337 (2014)
51_01B.SG.11.11SG_HM021	JN029801	All	Ng, O.T.	<i>ARHR</i> <b>28</b> (5); 527-30 (2012)
52_01B.MY.03.03MYKL018_1	DQ366664	All	Tee, K.K.	<i>JAIDS</i> <b>43</b> (5):523-529 (2006)
53_01B.MY.11.11FIR164	JX390610	All	Chow, W.Z.	<i>J Virol</i> <b>86</b> (20):11398-11399 (2012)
54_01B.MY.09.09MYSB023	JX390976	All	Ng, K.T.	<i>J Virol</i> <b>86</b> (20):11405-11406 (2012)
55_01B.CN.10.HNCS102056	JX574661	All	Han, X.	<i>Genome Announc</i> <b>1</b> (1):E00050-12 (2013)
56_cpx.FR.10.URF5_patient_A	JN882655	All	Leoz, M.	<i>AIDS</i> <b>25</b> (11):1371-1377 (2011)
57_BC.CN.09.09YNLX19sg	KC899008	All	Han, X.	<i>PLoS ONE</i> <b>8</b> (5):E65337 (2013)
58_01B.MY.09.09MYPR37	KC522031	All	Chow, W.Z.	<i>PLoS ONE</i> <b>9</b> (1):E85250 (2014)
59_01B.CN.09.09LNA423	JX960635	All	An, M.	<i>J Virol</i> <b>86</b> (22); 12402-6 (2012)
60_BC.IT.11.BAV499	KC899079	All	Simonetti, F.R.	<i>Infect Genet Evol</i> <b>2014</b> Apr;23:176-81 doi: 101016/j.meegid.2014.02.007 Epub 2014 Mar 3
61_BC.CN.10.JL100010	KC990124	All	Li, X.	<i>Genome Announc</i> <b>2013</b> Jun 27;1(3) pii: e00326-13 doi: 101128/genomeA00326-13
62_BC.CN.10.YNFL13	KC870034	All	Wei, H.	<i>ARHR</i> <b>30</b> (4):380-383 (2014)
63_02A1.RU.10.10RU6637	JN230353	All	Baryshev, P.B.	<i>Arch Virol</i> <b>157</b> (12); 2335-41 (2012)
64_BC.CN.09.YNFL31	KC870042	All	Hsi, J.	<i>ARHR</i> <b>30</b> (4); 389-93 (2014)
65_cpx.CN.10.YNFL01	KC870027	All	Feng, Y.	<i>ARHR</i> <b>30</b> (6); 598-602 (2014)
67_01B.CN.11.ANHUI_HF115	KC183779	All	Wu, J.	<i>PLoS ONE</i> <b>8</b> (1):E54322 (2013)
68_01B.CN.11.ANHUI_WH73	KC183782	All	Wu, J.	<i>PLoS ONE</i> <b>8</b> (1):E54322 (2013)
69_01B.JP.05.05JPMYC113SP420	LC027100	All	Kusagawa, S.	<i>Genome Announc</i> <b>2015</b> May 28;3(3) pii: e00196-15 doi: 101128/genomeA00196-15
70_BF1.BR.10.10BR_PE004	KJ849758	All	Pessoa, R.	<i>PLoS One</i> <b>9</b> (11); e112674 (2014)
71_BF1.BR.10.10BR_PE008	KJ849759	All	Pessoa, R.	<i>PLoS One</i> <b>9</b> (11); e112674 (2014)
72_BF1.BR.10.10BR_MG002	KJ671534	All	Pessoa, R.	<i>Genome Announc</i> <b>2</b> (3):e00386-14 (2014)
73_BG.DE.01.9196_01	AY882421	All	Harris, B.	<i>ARHR</i> <b>21</b> (7):654-660 (2005)
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85_BC.CN.14.14CN_SCYB2	KU992929	All	Su, L.	<i>ARHR</i> <b>2016</b> Jun 13
86_BC.CN.13.15YNHS18	KX582249	All	Li, Y.	<i>ARHR</i> <b>2016</b> Oct 18
87_cpx.CN.12.DH32	KF250408	All	Wei, H.	<i>Sci Rep</i> <b>2015</b> Jul 2;5:11323 doi: 101038/srep11323
88_BC.CN.05.05YNRL25sg	KC898979	All	Han, X.	<i>PLoS ONE</i> <b>8</b> (5):E65337 (2013)
O.CM.96.LA51YBF35	KU168294	All	Berg, M.G.	<i>J Clin Microbiol</i> <b>54</b> (4); 868-82 (2016)
O.CM.96.LA52YBF39	KU168295	All	Berg, M.G.	<i>J Clin Microbiol</i> <b>54</b> (4); 868-82 (2016)
O.CM.99.99CMU4122	AY169815	All	Yamaguchi, J.	<i>ARHR</i> <b>19</b> (11):979-988 (2003)
O.CM.x.pCMO2_3	AY618998	All	Tebit, D.M.	<i>Virology</i> <b>326</b> (2):329-339 (2004)
O.ES.01.Read25_HIV_GroupO	KX228804	All	Ragupathy, V.	Unpublished
O.FR.06.LA55RBF206	KU168298	All	Berg, M.G.	<i>J Clin Microbiol</i> <b>54</b> (4); 868-82 (2016)
O.GA.11.11Gab6352	JX245015	All	Liegeois, F.	<i>ARHR</i> <b>29</b> (7); 1085-90 (2013)
O.SN.99.99SE_MP1299	AJ302646	All	Toure-Kane, C.	<i>ARHR</i> <b>17</b> (12):1211-1216 (2001)
O.SN.99.99SE_MP1300	AJ302647	All	Toure-Kane, C.	<i>ARHR</i> <b>17</b> (12):1211-1216 (2001)
O.US.10.LTNP	JN571034	All	Buckheit, R.W.3.	<i>ARHR</i> <b>30</b> (6); 511-513 (2014)
N.CM.06.U14296	GQ324962	All	Vallari, A.	<i>ARHR</i> <b>26</b> (1):109-115 (2010)
N.FR.11.N1_FR_2011	JN572926	All	Delaugerre, C.	<i>Lancet</i> <b>378</b> (9806); 1894 (2011)
P.CM.06.U14788	HQ179987	All	Vallari, A.	<i>J Virol</i> <b>85</b> (3); 1403-7 (2011)
P.FR.09.RBF168	GU111555	All	Plantier, J.-C.	<i>Nat Med</i> <b>15</b> (8); 871-2 (2009)
CPZ.TZ.06.TAN5	JN091691	All	Rudicell, R.S.	<i>J Virol</i> <b>85</b> (19); 9918-28 (2011)
CPZ.US.85.US_Marilyn	AF103818	All	Gao, F.	<i>Nature</i> <b>397</b> (6718):436-441 (1999)
GOR.CM.12.SIVgor_BQID2	KP004991	All	D'arc, M.	<i>PNAS USA</i> <b>112</b> (11); E1343-52 (2015)
GOR.CM.13.SIVgor_BPID15	KP004990	All	D'arc, M.	<i>PNAS USA</i> <b>112</b> (11); E1343-52 (2015)



	membrane binding	Gag start, p17 start	phosphorylation site
B.FR.83.HXB2	K-A-R-L-L-S-T-Q-K-A-N-T-K-V-M-D-N-Q-T-S-SN	MGARASVLSGGEIDRWEKIRLRPGGKKYKLVHIVASRELERFAVNPGLLETSEGRQLTGLQPSLQTSSEELRSYNTVATLYCVHORIEIKDKEALDKEIEEQNK...	AA...ADTG...HS...NO...V...128
A1.CM.08.886.24	K-A-R-R-M-L-L-S-T-Q-ME-A-N-T-K-F-DV-M-D-N-Q-T-S-SN		128
A1.CY.08.CY236	K-E-R-R-M-L-L-S-T-Q-ME-A-N-T-K-F-DV-M-D-N-Q-T-S-SN		133
A1.KE.11.DEM111KE002	K-A-Q-S-R-R-L-L-S-T-Q-ME-A-N-T-K-F-DV-M-D-N-Q-T-S-SN		128
A1.NG.10.18NG040248	K-A-Q-S-R-R-L-L-S-T-Q-ME-A-N-T-K-F-DV-M-D-N-Q-T-S-SN		128
A1.PK.14.DEM1114PK001	K-A-Q-S-R-R-L-L-S-T-Q-ME-A-N-T-K-F-DV-M-D-N-Q-T-S-SN		128
A1.RW.11.DEM111RW002	K-A-Q-S-R-R-L-L-S-T-Q-ME-A-N-T-K-F-DV-M-D-N-Q-T-S-SN		129
A1.UG.11.DEM110UG009	K-K-T-L-M-L-L-S-T-Q-ME-A-N-T-K-F-DV-M-D-N-Q-T-S-SN		129
A1.ZA.04.503.15344.T10.A1	K-K-Q-R-L-L-S-T-Q-ME-A-N-T-K-F-DV-M-D-N-Q-T-S-SN		135
A2.CM.01.01CM.1445MV	K-A-R-R-M-L-L-S-T-Q-ME-A-N-T-K-F-DV-M-D-N-Q-T-S-SN		124
A3.SN.01.DDI579	K-MK-Q-RI-L-L-S-T-Q-MQ-A-K-T-K-DV-I-N-Q-T-T-N-R		126
A4.CD.97.97CD.KCC2	K-S-R-M-L-L-S-T-Q-MR-SA-T-K-K-L-N-Q-T-T-SA-D-SR		128
A6.BY.13.PV85	I-K-T-RI-L-L-S-N-Q-E-T-K-VK-F-R-I-Q-T-T-S-SK-I		128
A6.CY.09.CY255	I-K-A-Q-R-L-L-S-N-Q-E-T-K-VK-F-R-I-Q-T-T-S-SK-I		128
A6.RU.11.11RU6950	I-K-A-Q-RI-L-L-S-N-Q-E-T-K-VK-F-R-I-Q-T-T-S-SK-I		127
A6.UA.12.DEM112UA014	I-R-Q-T-RI-L-L-S-N-Q-E-T-K-VK-F-R-I-Q-T-T-S-SK-I		128
B.BR.10.10BR.RJ032	K-G-R-L-L-S-T-Q-IE-T-K-F-I-V-H-K-V-E-AAA-AT-K-N-S		131
B.CA.07.502.1191.03	K-R-R-R-L-L-S-T-Q-I-T-K-F-V-E-S-V-AAA-AT-K-N-S		130
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B.CN.12.DEMB12CN006	K-K-R-C-Q-I-S-I-A-K-I-K-F-A-V-G-DV-R-C-R-E-I-K-DN		128
B.CU.14.14CU005	Q-N-Q-I-S-I-A-K-I-K-F-A-V-G-DV-R-C-R-E-I-K-DN		128
B.DE.13.366396	R-N-Q-R-L-L-S-T-Q-D-K-H-K-K-VV-DV-V-V-T-DGA-N-S		128
B.ES.14.ARP1295	R-N-Q-R-L-L-S-T-Q-D-K-H-K-K-VV-DV-V-V-T-DGA-N-S		129
B.FR.11.DEMB11FR001	R-N-Q-R-L-L-S-T-Q-D-K-H-K-K-VV-DV-V-V-T-DGA-N-S		128
B.HT.05.05HT.129389	K-K-S-R-L-L-S-T-Q-D-K-H-K-K-VV-DV-V-V-T-DGA-N-S		126
B.JP.12.DEMB12JP001	IN-K-S-L-A-K-M-A-F-V-V-S-N-N-S-S-S-S-S-S-S-S		128
B.KR.07.HP.18.07JHS10.3909	I-K-Q-R-L-L-S-T-Q-G-K-E-K-F-V-DV-R-V-AAT-N-NS-SPGNSSP		133
B.RU.11.11RU21	R-N-Q-R-L-L-S-T-Q-G-K-E-K-F-V-DV-R-V-AAT-N-NS-SPGNSSP		131
B.SE.12.SE600057	R-N-Q-R-L-L-S-T-Q-G-K-E-K-F-V-DV-R-V-AAT-N-NS-SPGNSSP		128
B.TH.10.DEMB10TH002	R-N-Q-R-L-L-S-T-Q-G-K-E-K-F-V-DV-R-V-AAT-N-NS-SPGNSSP		133
B.US.16.2609	R-N-Q-R-L-L-S-T-Q-G-K-E-K-F-V-DV-R-V-AAT-N-NS-SPGNSSP		126
C.BR.11.DEMC11BR035	R-K-T-R-E-C-M-M-L-L-N-LD-S-T-IK-A-TK-I-KK-VR-K-S-00-N-L-E-E-TDK-GK-I		125
C.CN.10.YNFL19	I-R-RK-A-R-R-M-L-L-S-T-Q-K-MK-A-T-K-F-E-VR-V-I-00-T-E-E-K-E-AD-EK		126
C.DE.10.622166	I-R-RK-A-R-R-M-L-L-S-T-Q-K-MK-A-T-K-F-E-VR-V-I-00-T-E-E-K-E-AD-EK		126
C.ES.14.ARP1298	I-R-RK-A-R-R-M-L-L-S-T-Q-K-MK-A-T-K-F-E-VR-V-I-00-T-E-E-K-E-AD-EK		126
C.ET.08.ET104	TTN-R-R-T-H-M-L-L-LD-S-S-SA-K-MK-A-T-T-K-AG-V-C-00-T-K-E-ADK-GK		126
C.IN.15.NIRT008	I-R-K-K-R-H-R-L-L-LD-S-S-SA-K-MK-A-T-T-K-AG-V-C-00-T-K-E-ADK-GK		125
C.MW.09.703010256.CH256.W96	I-R-K-K-R-H-R-L-L-LD-S-S-SA-K-MK-A-T-T-K-AG-V-C-00-T-K-E-ADK-GK		125
C.NG.10.10NG026523	I-R-K-K-R-H-R-L-L-LD-S-S-SA-K-MK-A-T-T-K-AG-V-C-00-T-K-E-ADK-GK		125
C.NP.11.11NP016	I-R-K-K-R-H-R-L-L-LD-S-S-SA-K-MK-A-T-T-K-AG-V-C-00-T-K-E-ADK-GK		125
C.PK.14.DEMC14PK009	I-R-EK-T-R-H-M-L-L-LD-S-S-SA-K-MK-A-T-T-K-AG-V-C-00-T-K-E-ADK-GK		126
C.SE.13.SE600311	I-K-K-S-R-K-H-M-L-L-LD-S-S-SA-K-MK-A-T-T-K-AG-V-C-00-T-K-E-ADK-GK		125
C.TZ.08.707010457.CH457.W8	S-I-R-EK-K-S-M-L-L-LD-S-S-SA-K-MK-A-T-T-K-AG-V-C-00-T-K-E-ADK-GK		124
C.US.11.17TB4.4G8	I-R-EK-A-K-H-M-L-L-LD-S-S-SA-K-MK-A-T-T-K-AG-V-C-00-T-K-E-ADK-GK		126
C.ZA.13.DEMC13ZA152	I-R-EK-K-R-M-L-L-LD-S-S-SA-K-MK-A-T-T-K-AG-V-C-00-T-K-E-ADK-GK		126
C.ZM.11.DEMC11ZM006	I-R-K-K-R-K-H-M-L-L-LD-S-S-SA-K-MK-A-T-T-K-AG-V-C-00-T-K-E-ADK-GK		126
D.BR.10.10BR.RJ108	K-A-R-L-L-S-T-Q-K-I-AI-K-N-L-V-AK-D-E-L-S-N-T-A-NN-S		128
D.CD.03.LA17MuBo	K-D-S-Q-L-S-T-Q-K-E-I-A-K-T-K-N-L-V-E-KV-E-I-Q-R-EA-N-S		128
D.CM.10.DEMD10CM009	K-Q-S-N-R-L-L-S-T-Q-AD-K-S-E-AIK-I-H-K-DV-E-K-I-R-EA-N-S		127
D.CY.06.CY163	R-K-T-H-Q-I-D-K-A-S-F-I-QAG-E-N-T-R-N-S-S-S-S		128
D.KE.11.DEMD11KE003	Q-T-A-S-R-M-L-L-S-T-Q-K-M-AV-K-F-W-EG-KV-T-R-N-S-S-S		127
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D.UG.11.DEMD11UG003	K-E-R-Q-R-R-L-L-S-T-Q-K-I-AI-IK-IK-F-E-KV-T-E-N-S		127
D.YE.02.02YE516	K-E-R-Q-R-R-L-L-S-T-Q-K-I-AI-IK-IK-F-E-KV-T-E-N-S		126
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F1.AR.02.ARE933	I-K-T-Q-R-M-L-L-LD-S-T-K-I-H-I-K-VV-Y-EK-S-L-K-00-T-VT-V-A-A		124
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F1.ES.02.ES.X845.4	K-D-Q-R-M-L-LD-S-T-K-I-H-I-K-VV-Y-EK-S-L-K-00-T-VT-V-A-A		125
F1.ES.11.VA0053.nfl	K-A-Q-R-L-LD-S-T-K-I-H-I-K-VV-Y-EK-S-L-K-00-T-VT-V-A-A		124
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F1.RU.08.D88.845	K-D-R-R-L-LD-S-T-K-I-H-I-K-VV-Y-EK-S-L-K-00-T-VT-V-A-A		130
F2.CM.02.02CM.0016BBY	K-D-Q-R-L-L-LD-S-T-K-I-S-IK-I-K-F-A-VV-Y-Q-R-LQ-D-Y-00-T-P		122
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G.CM.08.709.10	K-A-Q-R-L-L-LD-S-T-K-I-S-IK-I-K-F-A-VV-Y-Q-R-LQ-D-Y-00-T-P		128
G.CM.10.DEMG10CM008	K-A-Q-R-L-L-LD-S-T-K-I-S-IK-I-K-F-A-VV-Y-Q-R-LQ-D-Y-00-T-P		128
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K.CM.96.96CM.MP535	K-A-Q-R-L-L-LD-S-T-K-I-S-IK-I-K-F-A-VV-Y-Q-R-LQ-D-Y-00-T-P		124
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01.AE.IR.10.10IR.THR48F	K-A-Q-R-L-L-LD-S-T-K-I-S-IK-I-K-F-A-VV-Y-Q-R-LQ-D-Y-00-T-P		128
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02.AG.DE.10.101114	K-A-Q-R-L-L-LD-S-T-K-I-S-IK-I-K-F-A-VV-Y-Q-R-LQ-D-Y-00-T-P		128
02.AG.GW.05.CC.0048	K-A-R-R-L-L-LD-S-T-K-I-S-IK-I-K-F-A-VV-Y-Q-R-LQ-D-Y-00-T-P		130



	p17 end_p24 start	CyPA binding	major homology region
B.FR.83.HXB2	.....SQNYPIVQNIQGQMVHQAISPRTLNAWKVKVEEKAFSPVEVIMPFMSALSEGATPDQLNTLMLNTVGGHQAAQMLKETINEEAAEWDVRVHPVHAGPIAPGQMRPRGSDIAGTTSTLQEOIGWMT.....NNPP...I.PVGEIYKRWILGLNKIVRMYSPTSILDIRQGPK		290
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A1.KE.11.DEMA111KE002	.....A.....I.....SL.....I.....M.....I.....D.....D.....L.....TQ.....P.....L.....P.....L.....G.....D.....D.....V.....K.....		290
A1.NG.10.10NG040248	.....A.....I.....SL.....I.....G.....N.....M.....I.....D.....D.....L.....V.....P.....I.....M.....VA.....S.....D.....D.....V.....K.....		290
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A3.SN.01.DDI579	.....A.....SL.....I.....T.....M.....I.....D.....D.....M.....P.....P.....S.....V.....R.....V.....K.....		288
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A6.CY.09.CY255	.....A.....IY.SM.....I.....G.....G.....M.....I.....D.....D.....L.....TQ.....FQ.....D.....N.....S.....D.....D.....V.....K.....		290
A6.RU.11.11RU6950	.....A.....I.....SM.....I.....T.....M.....I.....D.....D.....L.....AQ.....FP.....S.....D.....D.....K.....I.....H.....T.....V.....E.....K.....		286
A6.UA.12.DEMA112UA014	.....A.....SM.....I.....N.....I.....D.....D.....L.....AQ.....FP.....S.....D.....D.....K.....I.....H.....T.....V.....E.....K.....		290
B.BR.10.10BR.RJ032	.....L.....L.....I.....I.....D.....D.....L.....A.....A.....I.....Q.....S.....D.....D.....V.....K.....		293
B.CA.07.502.1191.03	.....L.....L.....I.....I.....D.....D.....L.....Q.....V.....D.....H.....S.....D.....D.....V.....K.....		292
B.CH.08.M2.0803101.NFLG8	.....L.....L.....I.....I.....D.....D.....L.....V.....V.....D.....H.....S.....D.....D.....V.....K.....		290
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B.DE.13.366396	.....L.....L.....I.....I.....D.....D.....L.....V.....V.....D.....H.....S.....D.....D.....V.....K.....		290
B.ES.14.ARP1495	.....H.....M.....I.....I.....D.....D.....L.....V.....V.....D.....H.....S.....D.....D.....V.....K.....		291
B.FR.11.DEMB11FR001	.....L.....L.....I.....I.....D.....D.....L.....V.....V.....D.....H.....S.....D.....D.....V.....K.....		290
B.HT.05.05HT.129389	.....M.....T.....I.....I.....D.....D.....L.....V.....V.....D.....H.....S.....D.....D.....V.....K.....		288
B.JP.12.DEMB12JP001	.....L.....L.....I.....I.....D.....D.....L.....V.....V.....D.....H.....S.....D.....D.....V.....K.....		290
B.KR.07.HP.18.07JHS10.3909	.....L.....L.....I.....I.....D.....D.....L.....V.....V.....D.....H.....S.....D.....D.....V.....K.....		290
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B.US.16.2609	.....L.....L.....I.....I.....D.....D.....L.....V.....V.....D.....H.....S.....D.....D.....V.....K.....		295
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C.DE.10.622166	.....L.....L.....I.....I.....D.....D.....L.....V.....V.....D.....H.....S.....D.....D.....V.....K.....		287
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G.GH.03.03GH175G	.....L.....L.....I.....I.....D.....D.....L.....AQ.....PQ.....I.....V.....E.....R.....S.....D.....D.....V.....K.....	289	
G.GW.08.LA571mNe	.....L.....L.....I.....I.....D.....D.....L.....AQ.....PQ.....I.....V.....E.....R.....S.....D.....D.....V.....K.....	286	
G.KE.09.DEMG09KE001	.....V.....A.....P.....A.....V.....I.....D.....D.....L.....AQ.....PQ.....I.....V.....E.....R.....S.....D.....D.....V.....K.....	290	
G.NG.12.12NG060409	.....A.....A.....I.....R.....I.....D.....D.....L.....AQ.....PQ.....I.....V.....E.....R.....S.....D.....D.....V.....K.....	289	
H.CD.04.LA19KoSa	.....A.....P.....I.....R.....I.....D.....D.....L.....AQ.....PQ.....I.....V.....E.....R.....S.....D.....D.....V.....K.....	293	
H.CF.02.LA25LeM1	.....A.....P.....I.....R.....I.....D.....D.....L.....AQ.....PQ.....I.....V.....E.....R.....S.....D.....D.....V.....K.....	287	
H.GB.00.00GBAC4001	.....L.....L.....I.....I.....D.....D.....L.....AQ.....PQ.....I.....V.....E.....R.....S.....D.....D.....V.....K.....	290	
J.CD.03.LA26D1An	.....H.....L.....P.....L.....I.....G.....N.....I.....D.....D.....L.....V.....V.....D.....H.....S.....D.....D.....V.....K.....	290	
J.CD.07.970C.KTB147	.....L.....L.....I.....I.....D.....D.....L.....V.....V.....D.....H.....S.....D.....D.....V.....K.....	291	
J.SE.93.SE9280.7887	.....L.....L.....I.....I.....D.....D.....L.....V.....V.....D.....H.....S.....D.....D.....V.....K.....	290	
K.CD.97.97ZR.EQT811	.....L.....L.....I.....I.....D.....D.....L.....V.....V.....D.....H.....S.....D.....D.....V.....K.....	286	
K.CM.96.96CM.MP535	.....L.....L.....I.....I.....D.....D.....L.....V.....V.....D.....H.....S.....D.....D.....V.....K.....	286	
01.AE.AF.07.569M	.....A.....A.....PL.....G.....N.....S.....M.....I.....D.....D.....L.....P.....P.....I.....T.....S.....D.....D.....V.....K.....	290	
01.AE.CM.11.1156.26	.....A.....I.....PV.....G.....N.....M.....I.....D.....D.....L.....P.....P.....I.....T.....S.....D.....D.....V.....K.....	290	
01.AE.CN.12.DE00112CN011	.....A.....I.....PV.....G.....N.....M.....I.....D.....D.....L.....P.....P.....I.....T.....S.....D.....D.....V.....K.....	290	
01.AE.HK.04.HK001	.....A.....I.....SL.....G.....N.....M.....I.....D.....D.....L.....P.....P.....I.....T.....S.....D.....D.....V.....K.....	290	
01.AE.IR.10.10IR.THR48F	.....A.....L.....T.....PV.....G.....N.....M.....I.....D.....D.....L.....P.....P.....I.....T.....S.....D.....D.....V.....K.....	290	
01.AE.IP.11.DE00111JP003	.....L.....L.....I.....I.....D.....D.....L.....P.....P.....I.....T.....S.....D.....D.....V.....K.....	290	
01.AE.SE.11.SEG01018	.....RL.....A.....HP.....I.....IQ.....G.....K.....Y.....M.....I.....D.....D.....L.....P.....P.....I.....T.....S.....D.....D.....V.....K.....	294	
01.AE.TH.10.DE00110TH001	.....A.....A.....PL.....G.....N.....M.....I.....D.....D.....L.....P.....P.....I.....T.....S.....D.....D.....V.....K.....	290	
01.AE.TH.90.CM240	.....V.....A.....H.....PL.....G.....N.....M.....I.....D.....D.....L.....P.....P.....I.....T.....S.....D.....D.....V.....K.....	290	
01.AE.US.05.306163.FL	.....L.....L.....I.....I.....D.....D.....L.....P.....P.....I.....T.....S.....D.....D.....V.....K.....	286	
02.AG.CM.10.DEM0210CM013	.....F.....A.....V.....I.....T.....M.....I.....D.....D.....L.....P.....P.....I.....T.....S.....D.....D.....V.....K.....	292	
02.AG.DE.09.081114	.....F.....A.....V.....I.....T.....M.....I.....D.....D.....L.....P.....P.....I.....T.....S.....D.....D.....V.....K.....	292	
02.AG.GW.05.CC.0048	.....A.....I.....SM.....AI.....M.....I.....D.....D.....L.....P.....P.....I.....T.....S.....D.....D.....V.....K.....	292	



	major homology region	p24 end_p2 start	p2 end_p7 start	Zn motif	Zn motif	p7 end_p1 start									
B.FR.83.HXB2	EPFRDYVDRFYKTLRAEQASQEVKNWMTETLLVQNANPDKITLKALGPAAATLEEMMTACQVGGPGHKARVLAEAMSQVT.....	N.SA.T.IVM.QR...	GNFRNQ.RKIVKCFNGCKEGHTARNCRAPRKKGCWKCGKEGHQMKDC.T...E.RQ...	ANF		433									
A1.CM.08.886.24	F.V.T.H.S.R.TG.S	Q.T.S	P.G.I	L		431									
A1.CY.08.CY236	F.V.T.D.AQ.SG.S	H.A.N	G.K.I	L		436									
A1.KE.11.DEMA111KE002	F.V.CT.D.S.RG.G.S	V.N.V	KG.I	L		431									
A1.NG.10.10NG040248	F.A.T.D.G.R.G.S	G.A.S	GK.KI	L		431									
A1.PK.14.DEMA114PK001	F.A.T.D.G.R.TG.S	H.T.N	KG.KR	L	I	434									
A1.RW.11.DEMA111RW002	F.A.T.D.G.D.I.S.RG.G.S	H.T.S	KG.KR	L		432									
A1.UG.11.DEMA110UG009	F.C.T.G.D.S.R.SG.S	H.T.N	GG.Q.KI	Y		433									
A1.ZA.04.503.15344.T10_A1	F.T.G.D.I.RG.SG.S	Q.T.N	G.KR.I	L		438									
A2.CM.01.01CM.1445MV	F.T.D.D.RH.SG.S	S.TNQ.N.V	GP.KR.I	L		429									
A3.SN.01.DD1579	F.C.T.D.S.R.TG	H.T.N.V	G.KR.I	L		429									
A4.CD.97.97CD.KCC2	F.T.D.D.R.AG	A.IS.V.E.RRM	T.LKG	L		431									
A6.BY.13.PV85	F.T.D.R.G	T.N.K	S.GP.KR.I	L	T	432									
A6.CY.09.CY255	F.T.D.R.G	S.T.N.K	S.GP.R.I	L		431									
A6.RU.11.1RU6950	F.T.D.D.R.SG	A.N.K	S.GP.KR.I	L	R	437									
A6.UA.12.DEMA112UA014	F.T.D.R.SG	A.S.K	S.GP.KR.I	L		431									
B.BR.10.10BR.RJ032	F.T.R	G.A.N.V	K	I	R.Q	N	435								
B.CA.07.502.1191.03		P.G.N	K	T			435								
B.CH.08.M2.0803101.NFLG8		P	G	RT	I	A	432								
B.CN.12.DEMB12CN006		D	V	K	G	R	I	433							
B.CU.14.14CU005		D	X	G	N	S		433							
B.DE.13.366396		D		G				433							
B.ES.14.ARP1195		R	T	S	I			434							
B.FR.11.DEMB11FR001		R	T	S	I			433							
B.HT.05.05HT.129389		G						430							
B.JP.12.DEMB12JP001		G						433							
B.KR.07.HP.18.07JHS10.3909		G						433							
B.RU.11.11RU21		M						438							
B.SE.12.SEG00057		V	T	D	S	I		436							
B.TH.10.DEMB10TH002		V	D					433							
B.US.16.2609		T						438							
C.BR.11.DEMC11BR035	F.T.D.D.R.G	N	T.S	K	S	KGP.RTI	V	L	D	430					
C.CN.10.YNFL19	F.T.D.D.R.G.SI	AN	S.N.L			KGP.KR	I	K		428					
C.DE.10.622166	F.C.T.D.D.RG.TG	AN	S.N.LI			KGP.KR	I	K	R	428					
C.ES.14.ARP1198	F.T.D.D.R.G	AN	S.N.L			KGP.KR	I	K		429					
C.ET.08.ET104	F.T.D.D.R.G.S	AH	T.N.L			KGP.PI	I	K		430					
C.IN.15.NIRT008	I.F.T.D.D.RG.G.S	AN	T.N			KGP.KRP	I	K		428					
C.MW.09.703010256.CH256.w96	F.T.D.D.R.G.S	TN	T.N.L			KGT.R	I	K		428					
C.NG.10.10NG0820523	F.T.D.D.I.G.TG.S	AN	H.A.N			N.KGA.KR	I	K	R	429					
C.NP.11.11NP16	F.T.D.D.R.G.S	AN	S.A.L			KGP.KRTI	I	K		429					
C.PK.14.DEMC14PK009	F.T.D.D.R.G	T	A			S.KGP.KRTI	L	K	N	429					
C.SE.13.SEG000311	F.T.D.D.R.G	I.HAS	Q.C.V.V.LK	S	KGH	TI	I		HE.N	R.Q.MLE.I	GHQ	429			
C.TZ.08.707010457.CH457.w8	F.T.D.D.I.G.S	AN	KGT.KR	I	S	KGT.KR	I	L		R	428				
C.US.11.17TB4.4G8	F.A.D.D.I	N	T.S	K	S	KGP.KRTI	I	K	R		430				
C.ZA.13.DEMC13ZA152	F.T.D.D.R.G.S	AN	HP.S	K		KGP.R	I	K	R		431				
C.ZM.11.DEMC11ZM006	F.C.T.D.D.R.G.S	AN	H.A.N	K		KGA.KR	V	I	K	Q	430				
D.BR.10.10BR.RJ108		D									434				
D.CD.03.LA17MuBo		D	G	D							434				
D.CM.10.DEMD10CM009		D									431				
D.CY.06.CY163		D									433				
D.KE.11.DEMD11KE003		D	R		N	M	G	S			434				
D.KR.04.04KR8		D									428				
D.TZ.01.288		D									433				
D.UG.10.DEMD10UG004		D									434				
D.UG.11.DEMD11UG003		D									432				
D.YE.02.02YE516		G	D		M	G	S				432				
F1.A0.06.A0.06.ANG32	F.C.T.D.G.D										429				
F1.AR.02.ARE933	F.A.T.D.G.D										428				
F1.BR.10.10BR.RJ015	F.T.D.G.D										431				
F1.BR.11.DEMF11BR037	F.T.D.D.R.G.S	A	G.A.A.VLL	K	S	KG	I	K	R	R	429				
F1.CY.08.CY222	F.T.D.D.R.G	I	A								427				
F1.ES.02.ES.X845.4	F.T.D.D.R.G	Q	T.S	K							429				
F1.ES.11.VA0053.nfl	F.T.D.D.R.S	A	T.K.L.N	S	KG	I	T	I	K	R	E	428			
F1.FR.04.LA221.eRe	F.V.T.D.G.D										427				
F1.R0.03.LA20DUC1	F.V.T.D.G.D.I										430				
F1.RU.08.D88.845	F.CT.G.D.R										434				
F2.CM.02.02CM.0016BBY	F.T.G.D.G										426				
F2.CM.10.DEMF210CM007	F.T.G.D.G										428				
F2.CM.11.DEURF11CM026	F.T.G.D.G.S	I	KA								425				
G.CD.03.LA23L1Ed	F.A.T.G.D.A	R	G		N	AG	A	T	A	M	S	KGP.KRNI	L	R	432
G.CM.08.709.10	F.T.D.D.RG.SG													433	
G.CM.10.DEMG10CM008	F.T.D.D.RG.SG													433	
G.CM.10.DEURF10CM020	F.T.D.D.RG.SG													433	
G.CN.08.GX.2084.08	F.T.D.D.RG.TG	S	NAS	G	AA	K	S	KGP.RXI	L	R			430		
G.ES.14.ARP1201	F.T.D.R.G	I	AS	GAA	AA	K		GP.KRNI	L	R			435		
G.GH.03.03GH175G	F.A.T.D.H	I	S	TG	G	TS	N	KGP.KRNI	L	R			432		
G.GH.08.LA57MnE	F.A.T.D.D													428	
G.KE.09.DEMG09KE001	F.V.T.D.S.D													432	
G.NG.12.12NG060409	K.F.T.D													433	
H.CD.04.LA19KoSa	F.C.D.G.N	R	G	SV										437	
H.CF.02.LA25LeM1	F.C.D.D	R	Q	I	S									431	
H.GB.00.00GBAC4001	F.T.D													434	
J.CD.03.LA26D1An	F.A.T.D.D	R	SG											432	
J.CD.07.J.97DC.KTB147	F.A.T.D.D	R	AG		RVSS.R	FG	I	N	T	N	I			V	429
J.SE.93.5E9280.7887	F.A.T.D													432	
K.CD.97.97ZR.E0TB11	FRV.T	R	SG											428	
K.CM.96.96CM.MP535	F.T.D													428	
01.AE.AF.07.569M	F.T	RS	SG											431	
01.AE.CM.11.1156.26	F.T	S	TG											431	
01.AE.CN.12.DE00112CN011	F.T	S	TGV											431	
01.AE.HK.04.HK001	F.T	S	AG		N	AO	Q	T	V	XKG	KR	I	R	L	431
01.AE.IR.10.10IR.THR48F	F.T	S	SG		HTO									432	
01.AE.JP.11.DE00111JP003	F.T	X	TG											431	
01.AE.SE.11.SEG01018	F.T	S	TG		NAO									435	
01.AE.TH.10.DE00110TH001	F.T	S	TG		H	Q								431	
01.AE.TH.90.CM240	F.T	S	TG		HAO									431	
01.AE.US.05.306163.FL	F.T	S	RG	SG										428	
02.AG.CM.10.DEM0210CM013	F.T	S	R	G										433	
02.AG.DE.10.021114	I.F.T	S	R	G										433	
02.AG.GW.05.CC.0048	I.F.T	M	RG	G										433	

	major homology region	p24 end_p2 start	p2 end_p7 start	Zn motif	Zn motif	p7 end_p1 start
B. FR. 83. HXB2	EPFRDYVDRFYKTLRAEQASQEVKNWMTETLLVQNPDPCKITLKALGPAAATLEEMMTACQGGVGGPKARVLAEMSQVT	.....	N.SA.T.IYM.QR	GNFRNQ	RKIVKCFNCGKEGHTARNCRAPRKKGCWKCGKEGHQMKDC	T...E.RQ...ANF
02 AG.KR.12.12MHI11 10746	F	T	S	R	G	Q
02 AG.KR.12.12MHR9	FR	T	S	R	G	Q
02 AG.LR.x.P0C44951	F	T	S	R	G	Q
02 AG.NG.12.12NG060418	F	T	RG	G	I	Q
02 AG.NG.x.IBNS	F	T	S	R	G	Q
02 AG.SG.x.EF02024	F	I	T	D	S	AQ
02 AG.SN.13.9580	F	T	D	S	R	G
03 AB.RU.97.KAL153 2	F	T	D	S	R	G
04 cpx.CY.94.94CY032 3	F	C	T	S	R	G
05 DF.BE.x.VT110	F	T	D	S	R	G
06 cpx.AU.96.BFP90	F	T	D	S	R	G
07 BC.CN.98.98CN009	F	T	D	S	R	G
08 BC.CN.97.97CNGX 6F	F	T	D	S	R	G
09 cpx.GH.96.96GH2911	F	T	D	S	R	G
10 CD.TZ.96.96TZ BF061	F	T	D	S	R	G
11 cpx.CM.95.95CM 1816	F	T	D	S	R	G
12 BF.AR.99.ARMA159	F	T	D	S	R	G
13 cpx.CM.96.96CM 1849	F	T	D	S	R	G
14 BG.ES.05.X1870	F	T	D	S	R	G
15 01B.TH.99.99TH MU2079	F	T	D	S	R	G
16 AZD.FR.97.97KR00	F	T	D	S	R	G
17 BF.AR.99.ARMA038	F	T	D	S	R	G
18 cpx.CU.99.CU76	F	T	D	S	R	G
19 cpx.CU.99.CU7	F	T	D	S	R	G
20 BG.CE.99.CE103	F	T	D	S	R	G
21 AZD.FR.97.97KR00	F	T	D	S	R	G
22 01A1.CM.01.01CM 0001BBY	F	T	D	S	R	G
23 BG.CU.03.CB118	F	T	D	S	R	G
24 BG.ES.08.X2456 2	F	T	D	S	R	G
25 cpx.CM.02.1918LE	F	T	D	S	R	G
26 AU.CD.02.02CD MBT047	F	T	D	S	R	G
27 cpx.FR.04.04FR K25	F	T	D	S	R	G
28 BF.BR.99.BREPM12609	F	T	D	S	R	G
29 BF.BR.01.BREPM16704	F	T	D	S	R	G
31 BC.BR.04.04BR142	F	T	D	S	R	G
32 06A1.EE.01.EE0369	F	T	D	S	R	G
33 01B.ID.07.07KT189 C	F	T	D	S	R	G
34 01B.TH.99.09TR1969P	F	T	D	S	R	G
35 AD.AF.07.169H	F	V	T	G	S	AQ
36 cpx.CM.00.00CMNYU830	F	V	T	D	S	R
37 cpx.CM.00.00CMNYU926	F	V	T	D	S	R
38 BF1.UY.03.UY03 3389	F	VV	ST	D	S	R
39 BF.BR.04.04BR3179	F	T	D	S	R	G
40 BF.BR.05.05BRJ055	F	T	D	S	R	G
42 BF.LU.03.LuBF 01 03	F	T	D	S	R	G
43 02G.SA.03.J11223	F	T	D	S	R	G
44 BF.CL.00.CH80	F	T	D	S	R	G
45 cpx.FR.04.04FR AUK	F	T	D	S	R	G
46 BF.BR.07.07BR FPS625	F	T	D	S	R	G
47 BF.ES.08.P1942	F	V	T	D	S	R
48 01B.MY.07.07MYKT021	F	T	D	S	R	G
49 cpx.GM.03.N26677	F	T	D	S	R	G
50 A10.GB.10.12792	F	T	D	S	R	G
51 01B.SG.10.125G HM021	F	T	D	S	R	G
52 01B.MY.03.03MYKL018 1	F	T	D	S	R	G
53 01B.MY.11.11FIR164	F	T	D	S	R	G
54 01B.MY.09.09MYSB023	F	T	D	S	R	G
55 01B.CN.10.HNCS102056	F	T	D	S	R	G
56 cpx.FR.10.10F5 patient A	F	T	D	S	R	G
57 BC.CN.09.09YNLX195g	S	F	T	D	S	R
58 01B.MY.09.09MYPR37	F	T	D	S	R	G
59 01B.CN.09.09LNA423	F	T	D	S	R	G
60 BC.IT.11.BAV499	F	T	D	S	R	G
61 BC.CN.10.J1100010	F	T	D	S	R	G
62 BC.CN.10.YNFL13	F	T	D	S	R	G
63 02A1.RU.10.10RU6637	F	T	D	S	R	G
64 BC.CN.09.YNFL31	F	T	D	S	R	G
65 cpx.CN.10.YNFL01	F	T	D	S	R	G
67 01B.CN.11.ANHUI HF115	F	T	D	S	R	G
68 01B.CN.11.ANHUI WH73	F	T	D	S	R	G
69 01B.JP.05.05JPMYC113SP420	F	T	D	S	R	G
70 BF1.BR.10.10BR PE004	F	A	K	T	G	D
71 BF1.BR.10.10BR PE008	F	T	D	S	R	G
72 BF1.BR.10.10BR MG002	F	T	D	S	R	G
73 BG.DE.01.01B5 01	F	T	D	S	R	G
74 01B.MY.10.10MYPR268	F	T	D	S	R	G
78 cpx.CN.13.YNCT19	F	T	D	S	R	G
85 BC.CN.14.14CN SCYB2	F	T	D	S	R	G
86 BC.CN.13.15YNS18	F	T	D	S	R	G
87 cpx.CN.12.DH32	F	T	D	S	R	G
88 BC.CN.05.05YNL255g	F	T	D	S	R	G
0.CM.96.LA51YBF35	F	T	D	S	R	G
0.CM.96.LA52YBF39	F	T	D	S	R	G
0.CM.99.99CMU4122	F	T	D	S	R	G
0.CM.x.pCM02 3	F	T	D	S	R	G
0.ES.01.Read1 HTV Group0	F	T	D	S	R	G
0.FR.06.LA55RBF206	F	T	D	S	R	G
0.GA.11.11Gabb6352	F	T	D	S	R	G
0.SN.99.99SE MP1299	F	T	D	S	R	G
0.SN.99.99SE MP1300	F	T	D	S	R	G
0.US.10.LTNP	F	T	D	S	R	G
0.CM.06.U14296	R	X	D	S	R	G
N.FR.11.W1.FR 2011	F	T	D	S	R	G
P.CM.06.U14788	F	T	D	S	R	G
P.FR.09.RBF168	F	T	D	S	R	G
CPZ.TZ.06.TAN5	I	P	H	Q	L	S
CPZ.US.85.US Marilyn	P	T	R	G	V	A
GOR.CM.12.SIVgor_BPID2	T	D	S	R	G	I
GOR.CM.13.SIVgor_BPID15	D	D	D	D	D	D



	p1 end	p6 start	Vpr binding	Vpr binding	p6 end	Gag end																
B. FR. 83. HXB2	LGKIWPS. YK	GRPNFLQ. SRPE	PTAPPE	ESFRSGVET	TTTP	Q	KQE	PI	DK	EL	YPLTSLRSLFQNDPSSQ*	500										
02 AG. KR. 12. 12MHI11 10746	N	P	Q	A	NLGM	E	I	SS	P	Q	R	G	YP	A	K	*	499					
02 AG. KR. 12. 12MHR9	S	P		A	LGM	E	I	S	P	Q	QREE	R	G	YP	A	K	*	499				
02 AG. LR. x. POC44951	S	P		A	GM	E	I	S	P		R	G	YP	A	K	*	495					
02 AG. NG. 12. 12NG060418	S	P		A	GM	E	I	S	P		R	G	YP	A	K	*	496					
02 AG. NG. x. IBNS	S	P		A	GM	E	I	S	P	Q	R	G	YP	A	K	*	495					
02 AG. SE. x. EF602024	H	P		A	GM	E	I	S	P		R	G	YP	A	K	*	495					
02 AG. SN. 13. 9580	R	F	S	KT	PFQSRTE												507					
03 AB. RU. 97. KAL153 2	R	S	P		S	A	N	GM	E	I	SS	L	OK	R	Q	HP	SI	K	D	L	499	
04 cpx. CY. 94. 94CY032 3	RM	S	N		A	CLERKE		SS	L		R	R	G	YP	A	K	S	L	501			
05 DF. BE. x. VT110	V	H		S	A	CLERKE		IASS	P		OK	E	E	E	E	Q	YP	A	K	S	L	503
06 cpx. AU. 96. BFP90	H	N		I	GF	EE		IA	S	P		SK	E	E	E	K	Q	S	*	500		
07 BC. CN. 98. 98CN009	H	N		I	GF	EE		IA	S	P		SK	E	E	E	K	Q	S	*	496		
08 BC. CN. 97. 97CNGX 6F	F	H		S	A	FEE		A	P		K	R	G	YP	A	K	S	L	490			
09 cpx. GH. 96. 96GH2911	S	P		S	A	GMRE		SS	X	X	K	R	G	YP	A	K	S	L	497			
10 CD. TZ. 96. 96TZ BF061	N			A	GF	EE		I	S	P	OK	E	E	E	E	K	Q	S	L	501		
11 cpx. CM. 95. 95CM 1816	N			A	GF	EE		I	S	P	OK	E	E	E	E	K	Q	S	L	499		
12 BF. AR. 99. ARMA159	N	N		A	GF	EE		I	SS	P	R	Q	E	GO	YP	A	K	S	*	494		
13 cpx. CM. 96. 96CM 1849	N			A	GF	EE		IA	S	P		K	ET		AA	K	S	*	508			
14 BG. ES. 05. X1870	R	S	P	N	L			IA	S	P		K	E	M		A	K	S	*	497		
15 01B. TH. 99. 99TH MU2079	RL			S	A	NWGM		SL	L		OK	R	H	TP	V	K	LL		498			
16 AZD. KR. 97. 97KR00	HS			A	D	GM					LK	NR	Q	HT	AI	K	S	*	499			
17 BF. AR. 99. ARMA038	N	N	T		A	GF	ET	I	Q	P		G	Q	YP	A	K	S	*	501			
18 cpx. CU. 99. CU76	N	K		A	LGF	EE		IA	S	P		SK	EE	K		F	S	K	S	L	497	
19 cpx. CU. 99. CU7	H			A	GF	EE		I	S	P		OK	E	D		A	K	S	L	501		
20 BG. CU. 99. CU103	L	H		A	GF	EE		IA	S	P	G	OK	E	D		T	K	S	*	497		
21 AZD. KE. 99. KER2003	S	P	G		A	M	GM		SS		OK	E	Q	PP	V	K	LL		499			
22 02A1. CM. 01. 01CM 0001B8Y	S	P		A	VGM	EE		I	SS	P		OK	E	Q	PP	V	K	LL		500		
23 BG. CU. 03. CB118	L	H		A	GF	EE		IA	S	P	G	K	EQ	D		I	K	S	*	498		
24 BG. ES. 08. X2456 2	L	H		A	GF	EE		IA	S	P	G	OK	E	D		I	K	S	*	497		
25 cpx. CM. 02. 1918LE	R	S	P	N	L			I	S	P		OK	E	Q	MA	K	S	*	499			
26 AU. CD. 02. 02CD MBT047	RF	N	P	LV		A	NLGM	EEG		SS	P	K	EG	Q	SP	T	K	S	L	496		
27 cpx. FR. 04. 04CD FR K25	SP	N		N		A	LM	SS		M	SS	P								497		
28 BF. BR. 99. BREPM12609	H	N		S	A	F	EE				OK	EE	G	YP	A	K	S	*	499			
29 BF. BR. 01. BREPM16704	H	N		S	A	LGF	EE	R	S	P		OK	E	GK	YP	A	K	S	*	510		
31 BC. BR. 04. 04BR142	R	H		S	A	FEE		R	S	P		OK	R		K	S	L		506			
32 06A1. EE. 01. EE0369	L	S	N	PTAPPASRL		A	FEE	AA	S	S		K	R		SA	K	S	*	495			
33 01B. ID. 07. JKT189 C	L	H		A	FEE						Q				VA	K	S	*	497			
34 01B. TH. 99. QUR1969P	F	N		A	T	EEG									SA	K	LL		498			
35 AD. AF. 07. 169H	NN	P	G		A	GF	EE	IK	S		OK	G							497			
36 cpx. CM. 00. 00CMNYU830	S	P		A	N	GI	EE	MSS		SR		G		YP	A	K	S	*	498			
37 cpx. CM. 00. 00CMNYU926	R	S	P		A	EVKE		VASS	L		G			YP	A	K	S	*	493			
38 BF1. UY. 03. UY03 3389	H			S	A	GF	EE	I	S	P	PKQEQ	OK	E	GM	YP	A	K	S	*	499		
39 BF. BR. 04. 04BR13179	N		T	PTA		A	GF	EE			R								502			
40 BF. BR. 05. 05BRJ055	P	N	N	L		A	GF	EE			OK	NE	G	YP	A	K	S	*	500			
42 BF. LU. 03. LuBF 01 03	C	N	PRPE		A	GF	EE	I	S	L	G	OK	E	G	CP				503			
43 02G. SA. 03. J11223	H			A	GF	EE		IA	S	P		R	E	S	P	A	K	S	*	498		
44 BF. CL. 00. CH80	N	P	N	L		A	GF	EE			OK	E	GK	YP	FA	K	S	*	496			
45 cpx. FR. 04. 04FR AUK	SR	P		S	A	GF	EE	I	SS	P		OK	E	G	YP	A	K	S	*	499		
46 BF. BR. 07. 07BR FPS625	H	N		S	A	EIR					OK	E	G	YP	A	K	S	*	496			
47 BF. ES. 08. P1942	S	N		A	LGF	EE					OK	E	G	YP	A	K	S	*	498			
48 01B. MY. 07. 07MYKT021	L	H	I		A	F	EE								A	S	*	499				
49 cpx. GM. 03. N26677	R	H		N		A	GF	EE		IA	S	P	QKE		SA	K	S	*	496			
50 A1D. GB. 10. 12792	H			A	GF	EE		VI	SS		OK				SA	K	LL		498			
51 01B. SG. 11. 11SG HM021	H			A	GF	EE							Q						499			
52 01B. MY. 03. 03MYK1018 1	N	P	X		A	NWGM		X	SS	L	QX		DP	PP	SV	K	S	LL	500			
53 01B. MY. 11. 11FIR164	L	X	H	N		F	EG												499			
54 01B. MY. 09. 09MYSB023	H			N		L	EE								VSA	K	S	*	501			
55 01B. CN. 10. HNC5102056	RL	N	P		A	DWGM		I	SS	P	OK		GH	RP	V	K	S	L	499			
56 cpx. FR. 10. URF5 patient A	N	P		A	VGM	EE		A	Y	P	R	OK	K	SRD	K	YP		S	L	500		
57 BC. CN. 09. 09YNLX195g	F	N		F	EE			X	A	P	LK	R							492			
58 01B. MY. 09. 09MYPR37	F	P	N		F	EE		X	A	P	G								498			
59 01B. CN. 09. 09LNA423	N	P		A	NWGM		S	L	L		OK		Q	HP	SI	K	S	L	492			
60 BC. IT. 11. BAV499	R	H		A	FEE						OK	R							491			
61 BC. CN. 10. J1100010	H			A	FEE		ASA	P			OK	R							492			
62 BC. CN. 10. YNFL13	H			A	FEE						SK	R							498			
63 02A1. RU. 10. 10RU6637	RL	NN	P		A	VGM	EE	I	SS	P	Q	R		G	YP	A	K	S	*	495		
64 BC. CN. 09. YNFL31	H			S	A	F	EE				GT				A	K	LC		496			
65 cpx. CN. 10. YNFL01	H		L		A	FEE		A	P	R	SK	R		G					495			
67 01B. CN. 11. ANHUI HF115	N		P		A	DWGM		I	SS	P	OK				H	V	K	L	497			
68 01B. CN. 11. ANHUI WH73	Y	N	P		A	DWGM		I	SS	P	OK		R		Q	V	K	L	495			
69 01B. JP. 05. 05JPMYC113SP420	H			S	L	EET		LT			D								K	497		
70 BF1. BR. 10. 10BR PE004	R	S	R	I	N			M	S	P	KKQE	OK	E	GR	YP	A	K	S	L	504		
71 BF1. BR. 10. 10BR PE008	RM	S	N	T		A	GF	EE			OK	SE		G	YP	A	K	S	L	499		
72 BF1. BR. 10. 10BR MG002	H	G	N	T		A	GF	EE			K	EE		G	YP	A	K	S	WL	501		
73 BG. DE. 01. 9196 01	H	N		A	GF	EE		IA	S	P		K		S					499			
74 01B. MY. 10. 10MYPR268	L	H		N		A	F	EE		A	T		N		SA	K	S	*	499			
78 cpx. CN. 13. YNFC19	H			N	PTAPPALQ. SRPE		V	F	EE		A	P		K	R				492			
85 BC. CN. 14. 14CN SCYB2	H			A	G	FEE		A	L	L		K	R		I				492			
86 BC. CN. 13. 15YHNS18	H			A	FEE						OK								492			
87 cpx. CN. 12. DH32	H			A	FEE						OK	R							499			
88 BC. CN. 05. 05YNRL255g	H			A	FEE						XX	R							495			
0. CM. 96. LA51YBF35	RY	P	GG	T	Y	KQVS		S	M	EVKRO	K	A	G	NOTOGG	Q							







	protease end_p66, p51 RT start	M41L	K70R D67N <sup>1</sup>	D110 catalytic site					
B. FR. 83. HXB2	IKVRQYDQLIEICGHKAIGTLVGP	TVNIIGRNLLTQIGCTLNFSPIS	ETVPVKLPGMDGPKVQWPLTE	EIKALVEICTEMEKEGKISKIG	PENYTPVFAIKKDKSTKWRKLV	DFRELNKRTQDFWEVQLGIPHP	AGLL. KKKKSVTVLVDGDAYF	SVPLDED	278
02 AG. KR. 12. 12MHI11 10746	-----K-----	M-----	-----	AN- A-	-----	-----	R-----	K-----	278
02 AG. KR. 12. 12MHR9	-----K-----	M-----	-----	TD-----	-----	-----	E-----	K-----	282
02 AG. LR. x. POC44951	-----P-----	M-----	L-----	TD- A-	-----	-----	E-----	K-----	278
02 AG. NG. 12. 12NG060418	-----N-----	M-----	-----	TA- E-	-----	D-----	-----	C-----	278
02 AG. NG. x. IBN5	-----K-----	M-----	-----	TD-----	-----	-----	-----	K-----	278
02 AG. SE. x. EF602024	-----K-----	M-----	-----	TD- A-	-----	-----	R-----	G-----	278
02 AG. SN. 13. 9580	-----A-----	M-----	L-----	L-----	-----	-----	I-----	R-----	286
03 AB. RU. 97. KAL153 2	-----K-----	M-----	-----	TD- K-	-----	-----	-----	G-----	278
04 cpx. CY. 94. 94CY032 3	-----P-----	M-----	L-----	T-----	-----	-----	I-----	-----	277
05 DF. BE. x. VT110	-----V-----	M-----	-----	T-----	-----	-----	I-----	-----	278
06 cpx. AU. 96. BFP90	-----K-----	M-----	I-----	T-----	-----	-----	R-----	-----	280
07 BC. CN. 98. 98CN009	-----E-----	M-----	L-----	TA- D-	-----	-----	I-----	-----	278
08 BC. CN. 97. 97CNGX 6F	-----E-----	M-----	L-----	TA- D-	-----	T-----	I-----	R-----	274
09 cpx. GH. 96. 96GH2911	-----E-----	M-----	-----	T-----	-----	-----	I-----	-----	277
10 CD. TZ. 96. 96TZ BF061	-----E-----	M-----	-----	T-----	-----	-----	I-----	-----	276
11 cpx. CM. 95. 95CM 1816	-----E-----	M-----	-----	VD-----	-----	-----	-----	-----	278
12 BF. AR. 99. ARMA159	-----K-----	M-----	L-----	I-----	-----	-----	-----	-----	278
13 cpx. CM. 96. 96CM 1849	-----N-----	M-----	-----	I-----	-----	-----	-----	-----	285
14 BG. ES. 05. X1870	-----M-----	M-----	-----	I-----	-----	-----	-----	-----	277
15 01B. TH. 99. 99TH MU2079	-----P-----	M-----	-----	T-----	-----	-----	I-----	-----	277
16 AZD. FR. 97. 97FR009	-----T-----	M-----	V-----	T-----	-----	-----	-----	-----	278
17 BF. AR. 99. ARMA038	-----K-----	M-----	L-----	T-----	-----	-----	-----	-----	278
18 cpx. CU. 99. CU76	-----P-----	M-----	-----	T-----	-----	-----	-----	-----	276
19 cpx. CU. 99. CU7	-----P-----	M-----	-----	T-----	-----	-----	-----	-----	277
20 BG. CU. 99. CU103	-----P-----	M-----	-----	T-----	-----	-----	-----	-----	274
21 AZD. KE. 99. KER2003	-----PL-----	M-----	-----	D-----	-----	-----	-----	-----	277
22 01A1. CM. 01. 01CM 0001BBY	-----P-----	M-----	-----	A-----	-----	I-----	-----	-----	278
23 BG. CU. 03. CB118	-----P-----	M-----	-----	-----	-----	-----	-----	-----	274
24 BG. ES. 08. X2456 2	-----E-----	M-----	-----	-----	-----	-----	-----	-----	274
25 cpx. CM. 02. 1918LE	-----E-----	M-----	-----	-----	-----	-----	-----	-----	277
26 AU. CD. 02. 02CD MBT047	-----V-----	M-----	-----	V-----	-----	-----	-----	-----	276
27 cpx. FR. 05. 94CD K25	-----E-----	M-----	-----	-----	-----	-----	-----	-----	278
28 BF. BR. 99. BREPM12609	-----K-----	M-----	-----	-----	-----	-----	-----	-----	278
29 BF. BR. 01. BREPM16704	-----K-----	M-----	-----	-----	-----	-----	-----	-----	278
31 BC. BR. 04. 04BR142	-----H-----	M-----	L-----	-----	-----	-----	-----	-----	284
32 06A1. EE. 01. EE0369	-----H-----	M-----	L-----	-----	-----	-----	-----	-----	278
33 01B. ID. 07. JKT189 C	-----P-----	M-----	-----	-----	-----	-----	-----	-----	278
34 01B. TH. 99. OUR1969P	-----K-----	M-----	L-----	-----	-----	-----	-----	-----	278
35 AD. AF. 07. 169H	-----K-----	M-----	-----	-----	-----	-----	-----	-----	277
36 cpx. CM. 00. 00CMNYU830	-----P-----	M-----	-----	-----	-----	-----	-----	-----	276
37 cpx. CM. 00. 00CMNYU926	-----P-----	M-----	-----	-----	-----	-----	-----	-----	276
38 BFI. UY. 03. UY03 3389	-----K-----	M-----	-----	-----	-----	-----	-----	-----	282
39 BF. BR. 04. 04BRJ3179	-----V-----	M-----	-----	-----	-----	-----	-----	-----	284
40 BF. BR. 05. 05BRRJ055	-----R-----	M-----	-----	-----	-----	-----	-----	-----	278
42 BF. LU. 03. LuBF 01 03	-----K-----	M-----	L-----	-----	-----	-----	-----	-----	282
43 02G. SA. 03. J11223	-----K-----	M-----	-----	-----	-----	-----	-----	-----	277
44 BF. CL. 00. CH80	-----K-----	M-----	-----	-----	-----	-----	-----	-----	278
45 cpx. FR. 04. 04FR AUK	-----K-----	M-----	-----	-----	-----	-----	-----	-----	278
46 BF. BR. 07. 07BR FPS625	-----K-----	M-----	-----	-----	-----	-----	-----	-----	278
47 BF. ES. 08. P1942	-----P-----	M-----	-----	-----	-----	-----	-----	-----	277
48 01B. MY. 07. 07MYKT021	-----P-----	M-----	-----	-----	-----	-----	-----	-----	278
49 cpx. GM. 03. N26677	-----ND-----	M-----	L-----	-----	-----	-----	-----	-----	276
50 A1D. GB. 10. 12702	-----V-----	M-----	-----	-----	-----	-----	-----	-----	276
51 01B. SG. 10. 125G HM021	-----V-----	M-----	-----	-----	-----	-----	-----	-----	278
52 01B. MY. 03. 03MYKL018 1	-----E-----	M-----	-----	-----	-----	-----	-----	-----	278
53 01B. MY. 11. 11FIR164	-----E-----	M-----	-----	-----	-----	-----	-----	-----	278
54 01B. MY. 09. 09MYSB023	-----P-----	M-----	-----	-----	-----	-----	-----	-----	278
55 01B. CN. 10. HNC5102056	-----P-----	M-----	-----	-----	-----	-----	-----	-----	278
56 cpx. FR. 10. URF5 patient A	-----SV-----	M-----	-----	-----	-----	-----	-----	-----	280
57 BC. CN. 09. 09YNLX1959	-----P-----	M-----	-----	-----	-----	-----	-----	-----	274
58 01B. MY. 09. 09MYPR37	-----P-----	M-----	-----	-----	-----	-----	-----	-----	278
59 01B. CN. 09. 09LNA423	-----C-----	M-----	-----	-----	-----	-----	-----	-----	275
60 BC. IT. 11. BAV499	-----A-----	M-----	-----	-----	-----	-----	-----	-----	273
61 BC. CN. 10. J1100010	-----P-----	M-----	-----	-----	-----	-----	-----	-----	274
62 BC. CN. 10. YNFL13	-----P-----	M-----	-----	-----	-----	-----	-----	-----	274
63 02A1. RU. 10. 10RU6637	-----M-----	M-----	-----	-----	-----	-----	-----	-----	278
64 BC. CN. 09. YNFL31	-----K-----	M-----	-----	-----	-----	-----	-----	-----	278
65 cpx. CN. 10. YNFL01	-----A-----	M-----	-----	-----	-----	-----	-----	-----	274
67 01B. CN. 11. ANHUI HF115	-----P-----	M-----	-----	-----	-----	-----	-----	-----	274
68 01B. CN. 11. ANHUI WH73	-----P-----	M-----	-----	-----	-----	-----	-----	-----	276
69 01B. JP. 05. 05JPMYC113SP420	-----P-----	M-----	-----	-----	-----	-----	-----	-----	276
70 BFI. BR. 10. 10BR PE004	-----K-----	M-----	-----	-----	-----	-----	-----	-----	280
71 BFI. BR. 10. 10BR PE008	-----K-----	M-----	-----	-----	-----	-----	-----	-----	278
72 BFI. BR. 10. 10BR MG002	-----K-----	M-----	-----	-----	-----	-----	-----	-----	278
73 BG. DE. 01. 9196 01	-----G-----	M-----	-----	-----	-----	-----	-----	-----	277
74 01B. MY. 10. 10MYPR268	-----K-----	M-----	-----	-----	-----	-----	-----	-----	278
78 cpx. CN. 13. YNTC19	-----K-----	M-----	-----	-----	-----	-----	-----	-----	287
85 BC. CN. 14. 14CN SCYB2	-----E-----	M-----	-----	-----	-----	-----	-----	-----	274
86 BC. CN. 13. 13YNHS18	-----P-----	M-----	-----	-----	-----	-----	-----	-----	274
87 cpx. CN. 12. DH32	-----V-----	M-----	-----	-----	-----	-----	-----	-----	274
88 BC. CN. 05. 05YNRL25sg	-----P-----	M-----	-----	-----	-----	-----	-----	-----	274
0. CM. 96. LA51YBF35	-----K-----	M-----	-----	-----	-----	-----	-----	-----	279
0. CM. 96. LA52YBF39	-----K-----	M-----	-----	-----	-----	-----	-----	-----	274
0. CM. 99. 99CMU4122	-----K-----	M-----	-----	-----	-----	-----	-----	-----	274
0. CM. x. pCM02 3	-----K-----	M-----	-----	-----	-----	-----	-----	-----	272
0. ES. 01. ReaD15 HTV Group0	-----K-----	M-----	-----	-----	-----	-----	-----	-----	274
0. FR. 06. LA55RBF206	-----K-----	M-----	-----	-----	-----	-----	-----	-----	276
0. GA. 11. 11Gabb6352	-----K-----	M-----	-----	-----	-----	-----	-----	-----	274
0. SN. 99. 99SE MP1299	-----K-----	M-----	-----	-----	-----	-----	-----	-----	274
0. SN. 99. 99SE MP1300	-----K-----	M-----	-----	-----	-----	-----	-----	-----	274
0. US. 10. LTNP	-----K-----	M-----	-----	-----	-----	-----	-----	-----	274
N. CM. 06. U14296	-----N-----	M-----	-----	-----	-----	-----	-----	-----	285
N. FR. 11. N1. FR 2011	-----N-----	M-----	-----	-----	-----	-----	-----	-----	285
P. CM. 06. U14788	-----K-----	M-----	-----	-----	-----	-----	-----	-----	275
P. FR. 09. RBF168	-----T-----	M-----	-----	-----	-----	-----	-----	-----	274
CPZ. TZ. 06. TAN5	-----V-----	M-----	-----	-----	-----	-----	-----	-----	274
CPZ. US. 85. US Marilyn	-----K-----	M-----	-----	-----	-----	-----	-----	-----	280
GOR. CM. 12. SIVgor B01D2	-----K-----	M-----	-----	-----	-----	-----	-----	-----	274
GOR. CM. 13. SIVgor BPID15	-----K-----	M-----	-----	-----	-----	-----	-----	-----	273



	polymerase motif M184V <sup>r</sup>				K219Q T215Y <sup>r</sup>				
B. FR. 83. HXB2									
02 AG. KR. 12. 12MHI1 10746	-	V	-	-	-	-	-	-	-
02 AG. KR. 12. 12MHR9	-	-	-	-	-	-	-	-	-
02 AG. LR. x. POC44951	-	-	-	-	-	-	-	-	-
02 AG. NG. 12. 12NG060418	-	-	-	-	-	-	-	-	-
02 AG. NG. x. 1BNG	-	-	-	-	-	-	-	-	-
02 AG. SE. x. 1E602024	-	-	-	-	-	-	-	-	-
02 AG. SN. 13. 9580	-	-	-	-	-	-	-	-	-
03 AB. RU. 97. KAL153 2	-	-	-	-	-	-	-	-	-
04 cpx. CY. 94. 94CY032 3	-	-	-	-	-	-	-	-	-
05 DF. BE. x. VT1110	-	-	-	-	-	-	-	-	-
06 cpx. AU. 96. BFP90	-	-	-	-	-	-	-	-	-
07 BC. CN. 98. 98CN009	-	-	-	-	-	-	-	-	-
08 BC. CN. 97. 97CNGX 6F	-	-	-	-	-	-	-	-	-
09 cpx. GH. 96. 96GH2911	-	-	-	-	-	-	-	-	-
10 CD. TZ. 96. 96TZ BF061	-	-	-	-	-	-	-	-	-
11 cpx. CM. 95. 95CM 1816	-	-	-	-	-	-	-	-	-
12 BF. AR. 99. ARMA159	-	-	-	-	-	-	-	-	-
13 cpx. CM. 96. 96CM 1849	-	-	-	-	-	-	-	-	-
14 BG. ES. 05. X1870	-	-	-	-	-	-	-	-	-
15 01B. TH. 99. 99TH MU2079	-	-	-	-	-	-	-	-	-
16 AZD. KR. 97. 97KR009	-	-	-	-	-	-	-	-	-
17 BF. AR. 99. ARMA038	-	-	-	-	-	-	-	-	-
18 cpx. CU. 99. CU76	-	-	-	-	-	-	-	-	-
19 cpx. CU. 99. CU7	-	-	-	-	-	-	-	-	-
20 BG. CU. 99. Cu103	-	-	-	-	-	-	-	-	-
21 AZD. KR. 99. KER2003	-	-	-	-	-	-	-	-	-
22 01A1. CM. 01. 01CM 0001BBY	-	-	-	-	-	-	-	-	-
23 BG. CU. 03. CB118	-	-	-	-	-	-	-	-	-
24 BG. ES. 08. X2456 2	-	-	-	-	-	-	-	-	-
25 cpx. CM. 02. 1918LE	-	-	-	-	-	-	-	-	-
26 AU. CD. 02. 02CD MBT047	-	-	-	-	-	-	-	-	-
27 cpx. FR. 04. 04FR K25	-	-	-	-	-	-	-	-	-
28 BF. BR. 99. BREPM12609	-	-	-	-	-	-	-	-	-
29 BF. BR. 01. BREPM16704	-	-	-	-	-	-	-	-	-
31 BC. BR. 04. 04BR142	-	-	-	-	-	-	-	-	-
32 06A1. EE. 01. EE0369	-	-	-	-	-	-	-	-	-
33 01B. ID. 07. JKT189 C	-	-	-	-	-	-	-	-	-
34 01B. TH. 99. 01B1969P	-	-	-	-	-	-	-	-	-
35 AD. AF. 07. 169H	-	-	-	-	-	-	-	-	-
36 cpx. CM. 00. 00CMNYU830	-	-	-	-	-	-	-	-	-
37 cpx. CM. 00. 00CMNYU926	-	-	-	-	-	-	-	-	-
38 BF1. UY. 03. UY03 3389	-	-	-	-	-	-	-	-	-
39 BF. BR. 04. 04BRJ3179	-	-	-	-	-	-	-	-	-
40 BF. BR. 05. 05BRJ055	-	-	-	-	-	-	-	-	-
42 BF. LU. 03. LuBF 01 03	-	-	-	-	-	-	-	-	-
43 02G. SA. 03. J11223	-	-	-	-	-	-	-	-	-
44 BF. CL. 00. CH80	-	-	-	-	-	-	-	-	-
45 cpx. FR. 04. 04FR AUK	-	-	-	-	-	-	-	-	-
46 BF. BR. 07. 07BR FPS625	-	-	-	-	-	-	-	-	-
47 BF. ES. 08. P1942	-	-	-	-	-	-	-	-	-
48 01B. MY. 07. 07MYKT021	-	-	-	-	-	-	-	-	-
49 cpx. GM. 03. N26677	-	-	-	-	-	-	-	-	-
50 A10. GB. 10. 10732	-	-	-	-	-	-	-	-	-
51 01B. SG. 11. 11SG HM021	-	-	-	-	-	-	-	-	-
52 01B. MY. 03. 03MYKL018 1	-	-	-	-	-	-	-	-	-
53 01B. MY. 11. 11FIR164	-	-	-	-	-	-	-	-	-
54 01B. MY. 09. 09MYSB023	-	-	-	-	-	-	-	-	-
55 01B. CN. 10. HNC5102056	-	-	-	-	-	-	-	-	-
56 cpx. FR. 10. 10FR patient A	-	-	-	-	-	-	-	-	-
57 BC. CN. 09. 09YNLX195g	-	-	-	-	-	-	-	-	-
58 01B. MY. 09. 09MYPR37	-	-	-	-	-	-	-	-	-
59 01B. CN. 09. 09LNA423	-	-	-	-	-	-	-	-	-
60 BC. IT. 11. BAV499	-	-	-	-	-	-	-	-	-
61 BC. CN. 10. J1100010	-	-	-	-	-	-	-	-	-
62 BC. CN. 10. YNFL13	-	-	-	-	-	-	-	-	-
63 02A1. RU. 10. 10RU6637	-	-	-	-	-	-	-	-	-
64 BC. CN. 09. YNFL31	-	-	-	-	-	-	-	-	-
65 cpx. CN. 10. YNFL01	-	-	-	-	-	-	-	-	-
67 01B. CN. 11. ANHUI HF115	-	-	-	-	-	-	-	-	-
68 01B. CN. 11. ANHUI WH73	-	-	-	-	-	-	-	-	-
69 01B. JP. 05. 05JPMYC113SP420	-	-	-	-	-	-	-	-	-
70 BF1. BR. 10. 10BR PE004	-	-	-	-	-	-	-	-	-
71 BF1. BR. 10. 10BR PE008	-	-	-	-	-	-	-	-	-
72 BF1. BR. 10. 10BR MG002	-	-	-	-	-	-	-	-	-
73 BG. DE. 01. 01B6 01	-	-	-	-	-	-	-	-	-
74 01B. MY. 10. 10MYPR268	-	-	-	-	-	-	-	-	-
78 cpx. CN. 13. YNTC19	-	-	-	-	-	-	-	-	-
85 BC. CN. 14. 14CN SCYB2	-	-	-	-	-	-	-	-	-
86 BC. CN. 13. 13YNHS18	-	-	-	-	-	-	-	-	-
87 cpx. CN. 12. DH32	-	-	-	-	-	-	-	-	-
88 BC. CN. 05. 05YNRL255g	-	-	-	-	-	-	-	-	-
0. CM. 96. LA51YBF35	-	-	-	-	-	-	-	-	-
0. CM. 96. LA52YBF39	-	-	-	-	-	-	-	-	-
0. CM. 99. 99CMU4122	-	-	-	-	-	-	-	-	-
0. CM. x. pCM02 3	-	-	-	-	-	-	-	-	-
0. ES. 01. Rea15 HIV Group0	-	-	-	-	-	-	-	-	-
0. FR. 06. LA55RBF206	-	-	-	-	-	-	-	-	-
0. GA. 11. 11Gab6352	-	-	-	-	-	-	-	-	-
0. SN. 99. 99SE MP1299	-	-	-	-	-	-	-	-	-
0. SN. 99. 99SE MP1300	-	-	-	-	-	-	-	-	-
0. US. 10. LTNP	-	-	-	-	-	-	-	-	-
N. CM. 06. U14296	-	-	-	-	-	-	-	-	-
N. FR. 11. N1. FR 2011	-	-	-	-	-	-	-	-	-
P. CM. 06. U14788	-	-	-	-	-	-	-	-	-
P. FR. 09. RBF168	-	-	-	-	-	-	-	-	-
CPZ. TZ. 06. TAN5	-	-	-	-	-	-	-	-	-
CPZ. US. 85. US Marilyn	-	-	-	-	-	-	-	-	-
GOR. CM. 12. SIVgor B0ID2	-	-	-	-	-	-	-	-	-
GOR. CM. 13. SIVgor BPID15	-	-	-	-	-	-	-	-	-

Accession	Sequence	Accession	Sequence	Accession	Sequence	Accession	Sequence
B.FR.83.HXB2	PLTEEALELAENREILKEPVHGVYDPSKDLIAEIQKGGQWYIYQIYQEPF.KNLKTKGYARMGAHTNDVKQLTEAVQKTTESIVIGWKTPKFKLPIQKMETWWTWEYQWATWPEWVFNTPLVLKLYOLEKEPIVGAETFFYVDGAANRETKLGKAGYVNRNG	p51 RT end_p15 RNase H start					
A1.CM.08.886_24	A-----D-----T-----V-----D-----K-----S-----R-----A-----V-----VV-----L-----D-----D-----D-----S-----D-----D-----						
A1.CY.08.CY236	T-----K-----D-----E-----V-----E-----L-----M-----D-----L-----D-----D-----D-----D-----D-----D-----D-----						
A1.KE.11.DEMA111KE002	T-----K-----D-----E-----V-----E-----L-----M-----D-----L-----D-----D-----D-----D-----D-----D-----D-----						
A1.NG.10.18NG040248	I-----E-----D-----D-----K-----K-----S-----V-----V-----VAQ-----V-----R-----R-----V-----D-----D-----D-----D-----D-----						
A1.PK.14.DEM114PK001	T-----D-----V-----D-----D-----L-----K-----K-----S-----V-----V-----VM-----A-----R-----RD-----MD-----D-----D-----D-----D-----D-----						
A1.RW.11.DEMA111RW002	T-----D-----V-----D-----D-----L-----K-----K-----S-----V-----V-----VM-----A-----R-----RD-----MD-----D-----D-----D-----D-----D-----						
A1.UG.11.DEMA110UG009	T-----D-----V-----D-----D-----L-----K-----K-----S-----V-----V-----VM-----A-----R-----RD-----MD-----D-----D-----D-----D-----D-----						
A1.ZA.04.503_15344_T10_A1	T-----D-----V-----D-----D-----L-----K-----K-----S-----V-----V-----VM-----A-----R-----RD-----MD-----D-----D-----D-----D-----D-----						
A2.CM.01.01CM_1445MV	R-----E-----N-----A-----T-----D-----D-----K-----K-----S-----V-----V-----VM-----A-----R-----RD-----MD-----D-----D-----D-----D-----D-----						
A3.SN.01.DDI579	T-----D-----A-----N-----D-----K-----K-----S-----R-----V-----V-----VV-----R-----R-----R-----M-----Y-----D-----D-----D-----D-----D-----						
A4.CD.97.97CD_KCC2	T-----D-----A-----N-----D-----K-----K-----S-----R-----S-----V-----VA-----R-----R-----R-----A-----M-----D-----D-----D-----D-----D-----						
A6.BY.13.PV85	T-----D-----D-----D-----K-----K-----G-----S-----R-----V-----V-----VA-----L-----R-----R-----R-----A-----M-----D-----D-----D-----D-----D-----						
A6.CY.09.CY255	T-----E-----V-----D-----D-----K-----K-----G-----S-----R-----V-----V-----VA-----L-----R-----R-----R-----A-----M-----D-----D-----D-----D-----D-----						
A6.RU.11.11RU6950	T-----R-----L-----V-----D-----D-----K-----K-----G-----S-----R-----V-----V-----VA-----L-----R-----R-----R-----A-----M-----D-----D-----D-----D-----D-----						
A6.UA.12.DEMA112UA014	T-----R-----L-----V-----D-----D-----K-----K-----G-----S-----R-----V-----V-----VA-----L-----R-----R-----R-----A-----M-----D-----D-----D-----D-----D-----						
B.BR.10.10BR_RJ032	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
B.CA.07.502_1191_03	T-----R-----T-----F-----L-----DH-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
B.CH.08.M2_0803101_NFLG8	SR-----T-----F-----L-----DH-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
B.CN.12.DEMB12CN006	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
B.CU.14.14CU005	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
B.DE.13.366396	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
B.ES.14.ARP1195	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
B.FR.11.DEMB11FR001	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
B.HT.05.05HT_129389	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
B.JP.12.DEMB12JP001	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
B.KR.07.HP_18_07JHS10_3909	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
B.RU.11.11RU21	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
B.SE.12.SEG00057	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
B.TH.10.DEMB10TH002	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
B.US.16.2609	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
C.BR.11.DEMC11BR035	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
C.CN.10.YNFL19	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
C.DE.10.622166	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
C.ES.14.ARP1198	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
C.ET.08.ET104	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
C.IN.15.NIRT008	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
C.MW.09.703010256_CH256.w96	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
C.NG.10.10NG026523	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
C.NP.11.11NP6	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
C.PK.14.DEMC14PK009	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
C.SE.13.SEG000311	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
C.TZ.08.707010457_CH457.w8	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
C.US.11.17TB4_4G8	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
C.ZA.13.DEM13ZA152	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
C.ZM.11.DEMC11ZM006	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
D.BR.10.10BR_RJ108	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
D.CD.03.LA17MuBo	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
D.CM.10.DEMD10CM009	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
D.CY.06.CY163	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
D.KE.11.DEMD11KE003	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
D.KR.04.04KR08	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
D.LZ.01.LZ88	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
D.UG.10.DEMD10UG004	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
D.UG.11.DEMD11UG003	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
D.YE.02.02YE516	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
F1.A0.06.A0_06_ANG32	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
F1.AR.02.ARE933	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
F1.BR.10.10BR_RJ015	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
F1.BR.11.DEMF11BR037	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
F1.CY.08.CY222	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
F1.ES.02.ES_X845_4	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
F1.ES.11.VA0053_nfl	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
F1.FR.04.LA221eRe	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
F1.FR.03.LA26DuCl	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
F1.RU.08.D88_845	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
F2.CM.02.02CM_0016BBY	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
F2.CM.10.DEMF210CM007	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
F2.CM.11.DEURF11CM026	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
G.CD.03.LA23LiEd	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
G.CM.08.709_10	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
G.CM.10.DEMG10CM008	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
G.CM.10.DEURF10CM020	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
G.CN.08.GX_2084_08	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
G.ES.14.ARP1201	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
G.GH.03.03GH1756	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
G.KE.08.LA571mMe	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
G.KE.09.DEMG09KE001	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
G.NG.12.12NG060409	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
H.CD.04.LA19KoSa	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
H.CF.02.LA25LeM1	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
H.GB.00.00GBAC4001	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
J.CD.03.LA26D1An	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
J.CD.07.J_970C_KTB147	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
J.SE.93.SEG280_7887	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
K.CD.97.97ZR_EQT811	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
K.CM.96.96CM_MP535	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
01.AE.AF.07.569M	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
01.AE.CM.11.1156_26	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
01.AE.CN.12.DE00112CN011	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
01.AE.HK.04.HK001	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
01.AE.IR.10.10IR_THR48F	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
01.AE.JP.11.DE00111JP003	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
01.AE.SE.11.SEG01018	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
01.AE.TH.10.DE00110TH001	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
01.AE.TH.90.CM240	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
01.AE.US.05.306163_FL	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
02.AG.CM.10.DEM0219CM013	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
02.AG.DE.09_081114	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						
02.AG.GW.05.CC_0048	T-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----						



p66 RT, p15 RNase H end, p31 Integrase start

B. FR. 83. HXB2	RQKVVTLTDDTTNQKTELQATYLAALQDSGLEVNIIVTDSQYALGIIAQPOOSESELVNIQIEQLIKKKEVYLWVPAHKIGGNEQDKLVSA	GIRKVLFLDGD	KAQD	.EHEKYHSNWRAMASDFNLPPVVAKEIVASCDKQCLKGEAMHQVDCSPGIWQLDCTHLEK	786
A1. CM. 08. 886 24	...I S E ... H H P ...	K D ... K E D S ...	V ...	E D ... T I ... I ...	786
A1. CY. 08. CY236	...S E ... H H S ...	K G D I S ...	T R ...	E D ... T G D I ... N ... M ...	783
A1. KE. 11. DEMA111KE002	...S E ... A H D S ...	R A ... K G D S ...	S ...	E D ... R T ... I ... N ...	785
A1. NG. 10. 10NG040248	...S E ... H H S ...	R S ... K A D S ...	S ...	E D ... R T ... I ... N ...	784
A1. PK. 14. DEMA114PK001	...S E ... H H S ...	R S ... K A D S ...	S ...	E D ... R T ... I ... N ...	785
A1. RW. 11. DEMA111RW002	K ... S E ... H L S ...	R D A V ... K E D S ...	S ...	E D ... R T ... I ... N ...	786
A1. UG. 11. DEMA110UG009	...S E ... H H S ...	R S ... K G D S ...	S ...	E D ... R T ... I ... N ...	786
A1. ZA. 04. 503 15344 T10_A1	...S E ... H H S ...	R S ... K E D S ...	S ...	E D ... R T ... I ... N ...	783
A2. CM. 01. 01CM 1445MV	I ... S E ... R H S ...	R ... F R I S ...	O R ...	E D ... R R T H ... I ... N ... I ...	786
A3. SN. 01. DDI579	S ... ME ... H H S ...	D I ... K E S ...	S ...	E D ... R R T ... I ...	785
A4. CD. 97. 97CD_KCC2	S ... E ... H H S ...	I ... K E S ...	S ...	E D ... R R T ... I ...	786
A6. BY. 13. PV85	P ... SE ... Q H H S ...	R ... I K K K R S ...	N ...	E D ... K ... I ...	787
A6. CY. 09. CY255	P ... E ... H H S ...	R ... I K K K R S ...	N ...	E D ... K ... I ...	786
A6. RU. 11. 11RU6950	P ... E ... H H S ...	R ... I K K K R S ...	N ...	E D ... K ... I ...	786
A6. UA. 12. DEMA112UA014	P ... E ... H H S ...	R ... I K K K R S ...	N ...	E D ... K ... I ...	786
B. BR. 10. 10BR_RJ032	P ... N ... H S ...	R ... S ...	S ...	E D ... R ...	785
B. CA. 07. 502 1191 03	I ... N ... H S ...	R ... S ...	S ...	E D ... R ...	786
B. CH. 08. M2 0803101_NFLG8	A ... I P ... Q H S ...	H ... K K S ...	N ... R I ...	D ... D ... N ... I ... I ... V ...	790
B. CN. 12. DEMB12CN006	S ... I ... H S ...	H ... K K S ...	T ... R ...	D ... N ... E ... I ... C ... Q ...	791
B. CU. 14. 14CU005	R ... P ... I ... H S ...	H ... K K S ...	S ...	D ... N ... E ... I ... C ... Q ...	786
B. DE. 13. 366396	R ... P ... I ... H S ...	H ... K K S ...	S ...	D ... N ... E ... I ... C ... Q ...	787
B. ES. 14. ARP1495	I ... S ... A ... H S ...	K ... X ... S ...	I ...	D ... K ... R ...	792
B. FR. 11. DEMB11FR001	I ... S ... H ... L S ...	K ... S ...	T ... R ...	D ... K ... R ...	785
B. HT. 05. 05HT 129389	K ... S ... H ... S ...	K ... S ...	E ... I ...	E D ... S ... R ... C ...	785
B. JP. 12. DEMB12JP001	K ... S ... H ... S ...	K ... S ...	S ...	E D ... K ... N ... I ... C ...	789
B. KR. 07. HP 18 07JHS10 3909	K ... S ... H ... S ...	K ... S ...	S ...	E D ... K ... N ... I ... C ...	785
B. RU. 11. 11RU219	S ... S ... H ... S ...	K ... S ...	S ...	E D ... K ... N ... I ... C ...	790
B. SE. 12. SE600057	S ... S ... H ... S ...	K ... S ...	S ...	E D ... K ... N ... I ... C ...	785
B. TH. 10. DEMB10TH002	S ... S ... H ... S ...	K ... S ...	S ...	E D ... K ... N ... I ... C ...	790
B. US. 16. 2609	I ... S ... H ... S ...	K ... S ...	S ...	E D ... K ... N ... I ... C ...	786
C. BR. 11. DEMC11BR035	I ... S ... E ... S ...	K ... T ... S ... L ... N ... R ... S ...	I ... N ...	E D ... N ... E ... I ... Q ... T ...	782
C. CN. 10. YNFL19	K ... I ... S ... E ... S ...	K ... K ... T ... N ... P ...	S ... V ...	E R ... D ... N ... F ... I ... I ...	786
C. DE. 10. 622166	I ... S ... E ... S ...	K ... K ... T ... N ... P ...	S ... V ...	E R ... D ... N ... F ... I ... I ...	789
C. ES. 14. ARP1498	T ... S ... E ... S ...	K ... D ... I ... T ...	O ... R ... S ...	E D ... N ... F ... I ... I ...	780
C. ET. 08. ET104	I ... S ... E ... S ...	K ... D ... I ... T ...	O ... R ... S ...	E D ... N ... F ... I ... I ...	786
C. IN. 15. NIRT008	I ... S ... V ... E ... S ...	K ... K ... I ... T ...	O ... R ... S ...	E D ... N ... F ... I ... I ...	782
C. MW. 09. 703010256_CH256.w96	S ... G ... G ... S ...	K ... K ... I ... T ...	O ... R ... S ...	E D ... N ... F ... I ... I ...	784
C. NG. 10. 10NG602523	I ... P ... DE ... S ...	K ... K ... I ... T ...	O ... R ... S ...	E D ... N ... F ... I ... I ...	784
C. NP. 11. 11NP016	I ... S ... E ... S ...	K ... K ... I ... T ...	O ... R ... S ...	E D ... N ... F ... I ... I ...	782
C. PK. 14. DEMC14PK009	S ... I ... SE ... S ...	K ... K ... I ... T ...	O ... R ... S ...	E D ... N ... F ... I ... I ...	782
C. SE. 13. SE600311	I ... S ... E ... S ...	K ... K ... I ... T ...	O ... R ... S ...	E D ... N ... F ... I ... I ...	797
C. TZ. 08. 707010457_CH457.w8	I ... S ... E ... S ...	H ... K ... I ... S ...	N ... O ... R ... S ...	E D ... N ... F ... I ... I ...	782
C. US. 11. 17TB4 4G8	I ... S ... E ... S ...	K ... K ... I ... S ...	N ... O ... R ... S ...	E D ... N ... F ... I ... I ...	796
C. ZA. 13. DEMC13ZA152	I ... S ... E ... S ...	K ... K ... I ... S ...	N ... O ... R ... S ...	E D ... N ... F ... I ... I ...	789
C. ZM. 14. DEMC14ZM006	I ... S ... E ... S ...	K ... K ... I ... S ...	N ... O ... R ... S ...	E D ... N ... F ... I ... I ...	787
D. BR. 10. 10BR_RJ108	S ... S ... N ... S ...	K ... S ... E ...	O ... R ... S ...	E D ... R ... N ... F ... I ...	788
D. CD. 03. LA17MuBo	A ... S ... F ... N ... N ... P ...	K ... S ... S ... L ...	O ... R ... S ...	E D ... R ... N ... F ... I ...	787
D. CM. 10. DEMD10CM009	A ... S ... F ... N ... N ... P ...	K ... S ... S ... L ...	O ... R ... S ...	E D ... R ... N ... F ... I ...	791
D. CY. 06. CY163	P ... F ... S ... N ... S ...	K ... S ... S ... L ...	O ... R ... S ...	E D ... R ... N ... F ... I ...	785
D. KE. 11. DEMD11KE003	S ... S ... N ... M ... S ...	K ... S ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	785
D. KR. 04. 04KR08	S ... S ... N ... S ...	K ... S ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	785
D. LZ. 01. 288	S ... S ... N ... S ...	K ... S ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	787
D. UG. 10. DEMD10UG004	P ... S ... A ... N ... N ... S ...	K ... D ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	785
D. UG. 11. DEMD11UG003	S ... S ... A ... N ... N ... S ...	K ... V ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	787
D. YE. 02. 02YE516	P ... F ... S ... N ... S ...	K ... V ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	787
F1. A0. 06. A0 06 ANG32	K E A P ... E ... A ... H ... S ...	K ... V ... S ... S ...	O ... R ... S ...	E D ... R ... N ... F ... I ...	790
F1. AR. 02. ARE933	A ... P ... E ... A ... K ... V ... S ...	K ... V ... S ... S ...	O ... R ... S ...	E D ... R ... N ... F ... I ...	786
F1. BR. 10. 10BR_RJ015	A ... S ... E ... A ... E ... O ... S ...	K ... V ... S ... S ...	O ... R ... S ...	E D ... R ... N ... F ... I ...	789
F1. BR. 11. DEMF11BR037	A ... S ... E ... A ... H ... S ...	K ... V ... S ... R ... O ... S ...	R ...	E D ... R ... N ... F ... I ...	786
F1. CY. 08. CY222	A ... S ... E ... A ... H ... S ...	K ... V ... S ... R ... O ... S ...	R ...	E D ... R ... N ... F ... I ...	785
F1. ES. 02. ES_X845 4	A ... S ... E ... A ... H ... O ... I ... A ... S ...	K ... K ... S ... R ... O ... T ... R ... I ... S ...	S ...	E D ... R ... N ... F ... I ...	788
F1. ES. 11. VA0053 nFl	A ... P ... E ... A ... H ... O ... I ... A ... S ...	K ... K ... S ... R ... O ... T ... R ... I ... S ...	S ...	E D ... R ... N ... F ... I ...	786
F1. FR. 04. LA221eRe	A ... S ... E ... A ... V ... H ... S ...	K ... H ... O ... I ... R ... I ... S ...	S ...	E D ... R ... N ... F ... I ...	787
F1. RO. 03. LA26DUC1	A ... S ... E ... A ... V ... H ... S ...	K ... H ... O ... I ... R ... I ... S ...	S ...	E D ... R ... N ... F ... I ...	788
F1. RU. 08. D88 845	A ... S ... E ... A ... V ... H ... S ...	K ... H ... O ... I ... R ... I ... S ...	S ...	E D ... R ... N ... F ... I ...	786
F2. CM. 02. 02CM 0016BBY	S ... S ... E ... H ... S ...	H ... L ... K ... S ...	S ...	E D ... R ... N ... F ... I ...	786
F2. CM. 10. DEMF210CM007	S ... S ... E ... H ... S ...	H ... L ... K ... S ...	S ...	E D ... R ... N ... F ... I ...	786
F2. CM. 11. DEURF11CM026	S ... S ... E ... H ... S ...	H ... L ... K ... S ...	S ...	E D ... R ... N ... F ... I ...	785
G. CD. 03. LA231Ed	K ... I ... I ... E ... A ... N ... P ...	R ... V ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	785
G. CM. 08. 709 10	K ... I ... I ... E ... A ... N ... P ...	R ... V ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	783
G. CM. 10. DEMG10CM008	K ... I ... I ... E ... A ... N ... P ...	R ... V ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	785
G. CM. 10. DEURF10CM020	K ... I ... I ... E ... A ... N ... P ...	R ... V ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	785
G. CN. 08. GX 2084 08	K ... I ... I ... E ... A ... H ... O ... S ...	R ... X ... X ... X ... I ... T ...	S ...	E D ... R ... N ... F ... I ...	790
G. ES. 14. ARP1201	K ... I ... I ... E ... A ... H ... O ... S ...	R ... X ... X ... X ... I ... T ...	S ...	E D ... R ... N ... F ... I ...	785
G. GH. 03. 03GH175G	K ... I ... I ... E ... A ... H ... O ... S ...	R ... X ... X ... X ... I ... T ...	S ...	E D ... R ... N ... F ... I ...	786
G. GW. 08. LA571mMe	K ... I ... I ... E ... A ... H ... O ... S ...	R ... X ... X ... X ... I ... T ...	S ...	E D ... R ... N ... F ... I ...	784
G. KE. 09. DEMG09KE001	K ... I ... I ... E ... S ... H ... O ... S ...	R ... D ... K ... R ... T ...	S ...	E D ... R ... N ... F ... I ...	784
G. NG. 12. 12NG060409	K ... I ... I ... E ... S ... H ... O ... S ...	R ... D ... K ... R ... T ...	S ...	E D ... R ... N ... F ... I ...	781
H. CD. 04. LA19KoSa	I ... I ... S ... E ... H ... S ...	K ... I ... F ... S ...	S ...	E D ... R ... N ... F ... I ...	784
H. CF. 02. LA25LeM1	I ... I ... S ... E ... H ... S ...	K ... I ... F ... S ...	S ...	E D ... R ... N ... F ... I ...	784
H. GB. 00. 00GBAC4001	K ... I ... S ... E ... H ... S ...	K ... I ... F ... S ...	S ...	E D ... R ... N ... F ... I ...	784
J. CD. 03. LA26D1An	S ... S ... E ... H ... S ...	R ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	784
J. CD. 07. J 970C_KTB147	S ... S ... E ... H ... S ...	R ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	783
J. SE. 93. SE9280 7887	S ... S ... E ... H ... S ...	R ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	784
K. CD. 97. 97ZR_E0TB11	I ... S ... I ... E ... A ... C ... S ...	K ... D ... R ... I ... S ...	S ...	E D ... R ... N ... F ... I ...	786
K. CM. 96. 96CM_MP535	S ... I ... E ... A ... C ... S ...	K ... D ... R ... I ... S ...	S ...	E D ... R ... N ... F ... I ...	786
01 AE. AF. 07. 569M	I ... E ... H ... H ... S ...	R ... V ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	786
01 AE. CM. 11. 1156 26	S ... AE ... H ... H ... S ...	R ... I ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	785
01 AE. CN. 12. DE00112CN011	R ... R ... I ... S ... S ...	R ... I ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	784
01 AE. HK. 04. HK001	R ... R ... I ... S ... S ...	R ... I ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	783
01 AE. IR. 10. 10IR_THR48F	K ... R ... S ... E ... H ... S ...	L ... V ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	778
01 AE. JP. 11. DE00111JP003	S ... S ... E ... H ... S ...	R ... V ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	784
01 AE. SE. 11. SE601018	S ... S ... E ... H ... S ...	R ... V ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	786
01 AE. TH. 10. DE00110TH001	S ... S ... E ... H ... S ...	R ... V ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	786
01 AE. TH. 90. CM240	S ... S ... E ... H ... S ...	R ... V ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	791
01 AE. US. 05. 306163 FL	S ... S ... E ... H ... S ...	R ... V ... S ... S ...	S ...	E D ... R ... N ... F ... I ...	784
02 AG. CM. 10. DEM0210CM013	R ... I ... S ... E ... H ... S ...	R ... D ... V ... S ...	S ...	E D ... R ... N ... F ... I ...	786
02 AG. DE. 09. 091114	I ... S ... E ... H ... S ...	R ... D ... V ... S ...	S ...	E D ... R ... N ... F ... I ...	786
02 AG. GW. 05. CC 0048	I ... S ... E ... H ... S ...	R ... D ... V ... S ...	S ...	E D ... R ... N ... F ... I ...	784





B. FR. 83. HXB2
02 AG. KR. 12. 12MHI11 10746
02 AG. KR. 12. 12MHR9
02 AG. LR. x. POC44951
02 AG. NG. 12. 12NG060418
02 AG. NG. x. 1BNG
02 AG. SE. x. 1E602024
02 AG. SN. 13. 9580
03 AB. RU. 97. KAL153 2
04 cpx. CY. 94. 94CY032 3
05 DF. BE. x. VT110
06 cpx. AU. 96. BFP90
07 BC. CN. 98. 98CN009
08 BC. CN. 97. 97CNG 6F
09 cpx. GH. 96. 96GH2911
10 CD. TZ. 96. 96TZ BF061
11 cpx. CM. 95. 95CM 1816
12 BF. AR. 99. ARMA159
13 cpx. CM. 96. 96CM 1849
14 BG. ES. 05. X1870
15 01B. TH. 99. 99TH MU2079
16 AZD. KR. 97. 97KR000
17 BF. AR. 99. ARMA038
18 cpx. CU. 99. CU76
19 cpx. CU. 99. CU7
20 BG. CU. 99. CU103
21 AZD. KE. 99. KEZ003
22 01A1. CM. 01. 01CM 0001BBY
23 BG. CU. 03. CB118
24 BG. ES. 08. X2456 2
25 cpx. CM. 02. 1918LE
26 AU. CD. 02. 02CD MBT0047
27 cpx. FR. 04. 04CD K25
28 BF. BR. 99. BREPM12609
29 BF. BR. 01. BREPM16704
31 BC. BR. 04. 04BR142
32 06A1. EE. 01. EE0369
33 01B. ID. 07. JKT189 C
34 01B. TH. 99. 01R1969P
35 AD. AF. 07. 169H
36 cpx. CM. 00. 00CMNYU830
37 cpx. CM. 00. 00CMNYU926
38 BF1. UY. 03. UY03 3389
39 BF. BR. 04. 04BR13179
40 BF. BR. 05. 05BRR1055
42 BF. LU. 03. LuBF 01 03
43 02G. SA. 03. J11223
44 BF. CL. 00. CH80
45 cpx. FR. 04. 04FR AUK
46 BF. BR. 07. 07BR FPS625
47 BF. ES. 08. P1942
48 01B. MY. 07. 07MYKT021
49 cpx. GM. 03. N26677
50 A10. GB. 10. 12792
51 01B. SG. 11. 11SG HM021
52 01B. MY. 03. 03MYKL018 1
53 01B. MY. 11. 11FIR164
54 01B. MY. 09. 09MYSB023
55 01B. CN. 10. HNC5102056
56 cpx. FR. 10. 10FR patient A
57 BC. CN. 09. 09YNLX195g
58 01B. MY. 09. 09MYPR37
59 01B. CN. 09. 09LNA423
60 BC. IT. 11. BAV499
61 BC. CN. 10. J1100010
62 BC. CN. 10. YNFL13
63 02A1. RU. 10. 10RU6637
64 BC. CN. 09. YNFL31
65 cpx. CN. 10. YNFL01
67 01B. CN. 11. ANHUI HF115
68 01B. CN. 11. ANHUI WH73
69 01B. JP. 05. 05JPMYC113SP420
70 BF1. BR. 10. 10BR PE004
71 BF1. BR. 10. 10BR PE008
72 BF1. BR. 10. 10BR MG002
73 06. DE. 01. 9195 01
74 01B. MY. 10. 10MYPR268
78 cpx. CN. 13. YNTC19
85 BC. CN. 14. 14CN SCYB2
86 BC. CN. 13. 13YNHS18
87 cpx. CN. 12. DH32
88 BC. CN. 05. 05YNRL25sg
0. CM. 96. LA51YBF35
0. CM. 96. LA52YBF39
0. CM. 99. 99CMU4122
0. CM. x. pCM02 3
0. ES. 01. Rea025 HTV Group0
0. FR. 06. LA55RBF206
0. GA. 11. 11Gabb6352
0. SN. 99. 99SE MP1299
0. SN. 99. 99SE MP1300
0. US. 10. LTNP
N. CM. 06. U14296
N. FR. 11. N1. FR 2011
P. CM. 06. U14788
P. FR. 09. RBF168
CPZ. TZ. 06. TAN5
CPZ. US. 85. US Marilyn
GOR. CM. 12. SIVgor B01D2
GOR. CM. 13. SIVgor\_BP1D15

Table with columns for protein sequence alignment. Rows correspond to the accession numbers listed on the left. The table contains amino acid sequences for various HIV-1 proteins, with some positions highlighted in bold or underlined. The sequences are aligned to show conserved regions across different strains.

	p31 Integrase end Pol end	
B. FR. 83. HXB2	LWKGEGAVVIQDNSDIKVVPRRKAKIIRDYGKQMGAGDCCVASRQDEE . . . . . *	
A1. CM. 08. 886 24	----- N ----- G -----	1003
A1. CY. 08. CY236	----- N ----- G -----	1004
A1. KE. 11. DEMA111KE002	----- G ----- LKH ----- G -----	1001
A1. NG. 10. 10NG040248	----- N ----- V ----- G -----	1003
A1. PK. 14. DEMA114PK001	----- N ----- V ----- G -----	1002
A1. RW. 11. DEMA111RW002	----- K ----- V ----- G -----	1003
A1. UG. 11. DEMA110UG009	----- E ----- H ----- G -----	1004
A1. ZA. 04. 503 15344 T10_A1	----- I ----- V ----- G -----	1004
A2. CM. 01. 01CM 1445MV	----- I ----- V ----- G -----	1001
A3. SN. 01. DDI579	----- I ----- V ----- G -----	1004
A4. CD. 97. 97CD_KCC2	----- I ----- V ----- G -----	1003
A6. BY. 13. PV85	----- N ----- V ----- G -----	1004
A6. CY. 09. CY255	----- N ----- V ----- G -----	1005
A6. RU. 11. 11RU6950	----- N ----- V ----- G -----	1004
A6. UA. 12. DEMA112UA014	----- N ----- V ----- G ----- A -----	1004
B. BR. 10. 10BR_RJ032	----- E ----- V ----- G -----	1003
B. CA. 07. 502 1191 03	----- E ----- V ----- G -----	1004
B. CH. 08. M2 0803101 NFLG8	----- V ----- V ----- G -----	1008
B. CN. 12. DEMB12CN006	----- E ----- V ----- G -----	1009
B. CU. 14. 14CU005	----- E ----- V ----- G -----	1004
B. DE. 13. 366396	----- E ----- V ----- G -----	1005
B. ES. 14. ARP1195	----- E ----- V ----- G -----	1010
B. FR. 11. DEMB11FR001	----- E ----- V ----- G -----	1003
B. HT. 05. 05HT 129389	----- E ----- V ----- G -----	1003
B. JP. 12. DEMB12JP001	----- V ----- V ----- M -----	1007
B. KR. 07. HP 18 07JHS10 3909	----- V ----- V ----- M -----	1003
B. RU. 11. 11RU21n	----- V ----- V ----- M -----	1008
B. SE. 12. SE600057	----- V ----- V ----- M -----	1003
B. TH. 10. DEMB10TH002	----- V ----- V ----- M -----	1008
B. US. 16. 2609	----- V ----- V ----- M -----	1004
C. BR. 11. DEMC11BR035	----- L ----- V ----- K ----- A ----- M -----	1000
C. CN. 10. YNFL19	----- X ----- K ----- A ----- G -----	1004
C. DE. 10. 622166	----- V ----- K ----- A ----- G -----	1006
C. ES. 14. ARP1198	----- V ----- K ----- A ----- G -----	998
C. ET. 08. ET104	----- V ----- K ----- A ----- M ----- G -----	1004
C. IN. 15. NIRT008	----- E ----- K ----- A ----- G -----	1000
C. MW. 09. 703010256 CH256.w96	----- K ----- K ----- A ----- G -----	1002
C. NG. 10. 10NG020523	----- K ----- K ----- A ----- G -----	1000
C. NP. 11. 11NP016	----- K ----- K ----- A ----- G -----	1000
C. PK. 14. DEMC14PK009	----- K ----- K ----- A ----- G -----	1000
C. SE. 13. SE6000311	----- K ----- K ----- A ----- G -----	1019
C. TZ. 08. 707010457 CH457.w8	----- K ----- V ----- KH ----- A ----- D -----	1004
C. US. 11. 17TB4 4G8	----- V ----- V ----- A ----- G -----	1014
C. ZA. 13. DEMC13ZA152	----- V ----- V ----- A ----- G -----	1007
C. ZM. 11. DEMC11ZM006	----- E ----- V ----- A ----- G -----	1009
D. BR. 10. 10BR_RJ108	----- E ----- V ----- G ----- G -----	1006
D. CD. 03. LA17MuBo	----- E ----- V ----- G ----- G -----	1005
D. CM. 10. DEMD10CM009	----- E ----- V ----- G ----- G -----	1009
D. CY. 06. CY163	----- V ----- V ----- G ----- G -----	1003
D. KE. 11. DEMD11KE003	----- S ----- V ----- G ----- G -----	1003
D. KR. 04. 04KR08	----- S ----- V ----- G ----- G -----	1003
D. TZ. 01. A288	----- H ----- V ----- G ----- G -----	1005
D. UG. 10. DEMD10UG004	----- E ----- V ----- G ----- G -----	1003
D. UG. 11. DEMD11UG003	----- E ----- V ----- G ----- G -----	1005
D. YE. 02. 02YE516	----- E ----- V ----- G ----- G -----	1005
F1. A0. 06. A0 06 ANG32	----- E ----- L ----- M ----- G -----	1008
F1. AR. 02. ARE933	----- E ----- L ----- M ----- G -----	1004
F1. BR. 10. 10BR_RJ015	----- E ----- L ----- M ----- G -----	1007
F1. BR. 11. DEMF11BR037	----- E ----- L ----- M ----- G -----	1004
F1. CY. 08. CY222	----- E ----- I ----- M ----- G -----	1003
F1. ES. 02. ES_X845 4	----- E ----- I ----- M ----- G -----	1006
F1. ES. 11. VA0053 nfl	----- E ----- I ----- M ----- G -----	1004
F1. FR. 04. LA22LeRe	----- E ----- I ----- M ----- G -----	1005
F1. RO. 03. LA20DuC1	----- E ----- I ----- M ----- G -----	1006
F1. RU. 08. D88 845	----- E ----- I ----- M ----- G -----	1004
F2. CM. 02. 02CM 0016BBY	----- NE ----- V ----- G ----- G -----	1004
F2. CM. 10. DEMF210CM007	----- NE ----- V ----- G ----- G -----	1004
F2. CM. 11. DEURF11CM026	----- K ----- V ----- G ----- G -----	1003
G. CD. 03. LA23LiEd	----- NE ----- R ----- L ----- S ----- G -----	1003
G. CM. 08. 789 10	----- NE ----- R ----- L ----- S ----- G -----	1001
G. CM. 10. DEMG10CM008	----- NE ----- R ----- L ----- S ----- G -----	1003
G. CM. 10. DEURF10CM020	----- E ----- R ----- L ----- S ----- G -----	1003
G. CN. 08. GX 2084 08	----- NE ----- R ----- L ----- S ----- G -----	1008
G. ES. 14. ARP1201	----- X ----- N ----- X ----- S ----- G -----	1003
G. GH. 03. 03GH175G	----- NE ----- K ----- S ----- G -----	1004
G. GW. 08. LAS7LmNe	----- NE ----- K ----- S ----- G -----	1002
G. KE. 09. DEMG09KE001	----- N ----- L ----- S ----- G -----	1002
G. NG. 12. 12NG060409	----- NE ----- L ----- S ----- G -----	999
H. CD. 04. LA19KoSa	----- E ----- Q ----- G ----- N -----	1002
H. CF. 02. LA25LeMi	----- E ----- Q ----- G ----- N -----	1002
H. GB. 00. 00GBAC4001	----- E ----- Q ----- G ----- N -----	1002
J. CD. 03. LA26D1An	----- E ----- Q ----- G ----- N -----	1002
J. CD. 07. J 970C_KTB147	----- E ----- Q ----- G ----- N -----	1001
J. SE. 93. SE9280 7887	P ----- E ----- Q ----- G ----- N -----	1002
K. CD. 97. 97ZR_E0TB11	# # ----- E ----- G -----	1001
K. CM. 96. 96CM_MP535	# # ----- E ----- G -----	1004
01. AE. AF. 07. 569M	----- E ----- G -----	1004
01. AE. CM. 11. 1156 26	----- E ----- G -----	1003
01. AE. CN. 12. DE00112CN011	----- E ----- G -----	1002
01. AE. HK. 04. HK001	----- E ----- G -----	1001
01. AE. IR. 10. 10IR_THR48F	----- E ----- G -----	996
01. AE. JP. 11. DE00111JP003	----- E ----- G -----	1002
01. AE. SE. 11. SE601018	----- E ----- G -----	1004
01. AE. TH. 10. DE00110TH001	----- E ----- G -----	1004
01. AE. TH. 90. CM240	----- E ----- G -----	1009
01. AE. US. 05. 306163 FL	----- E ----- G -----	1002
02. AG. CM. 10. DE00210CM013	----- E ----- G ----- T -----	1004
02. AG. DE. 10. 701114	----- E ----- G ----- T -----	1004
02. AG. GW. 05. CC_0048	----- K ----- G ----- N -----	1004



Vif start

MENRWQVMIVWQVDMRRTWKSLVKHHMYVSGKARWGFYRHYHESPHRISSEVHPIDG\_AR\_LVITTYWGLHTGERDWHLGGQVSIIEWRKKRYSTQVDPLEADQLIHLYYDFCDSDAIRKALLGHVSPRCEYQAG\_HN\_KVSLQYLAALALI...T\_PKKIKP

B.FR.83.HXB2	N	K	KK	L	D	R	KV	N	VR	Q	K	H	LRK	D	OV	S	A	T	K	V	A	TR
A1.CM.08.886_24		K	KR	KR																		
A1.CY.08.CY236		K	KR	KR																		
A1.KE.11.DEM111KE002		N	Y	R	R	KE	R	KV	E	I	V	Q	K	Q	H	L	I	D	DM	H	N	E
A1.NG.10.10NG040248		K	H			R	KE	R	KV	E	I	V	Q	K	Q	H	L	I	D	DM	H	N
A1.PK.14.DEM114PK001		H	I	Y		K	K	S	K	TR	V											
A1.RW.11.DEM111RW002		H	I	Y		K	K	S	K	TR	V											
A1.UG.11.DEM110UG009		N				K	K	K	F	R	KV	K	I	VR	N	Q	Q	H	LR	I	D	H
A1.ZA.04.503_15344_T10_A1		N				I	K	KN	F	RN	KVA	E	K	VR	N	Q	Q	H	LR	I	D	H
A2.CM.01.01CM_1445MV		N				I	R	KE	F	R	KV	E	IVR	P	KE	H	Q	K	I	D	H	H
A3.SN.01.DDI1579		N				I	K	DI	DCR	A	M	VR	P	Q	H	Q	I	D	H	H	R	I
A4.CD.97.97CD_KCC2		A	N			H	K	I	R	K	V											
A6.BY.13.PV85		H				I	H	I	KE	R	KV											
A6.CY.09.CY255		K				R	KE	C	R	V												
A6.RU.11.1RU6950						N																
A6.UA.12.DEM112UA014		Q	K	N		K	E	R	G	V												
B.BR.10.10BR_R1032		N				Y	I	H	K	KE	G	T	N	SK	VI							
B.CA.07.502_1191_03		N				I	K	N	D	T	N	K	A									
B.CH.08.M2_0803101_NFLG8		N				I	H	K	K	I	K	T	N	K	V							
B.CN.12.DEMB12CN006		N				R	K															
B.CU.14.14CU005		NA				I	K	KR	V	D												
B.DE.13.366396		NA				I	K	KR	V	D												
B.EC.14.ARP1198		N	I	Y	I	H	K	NR	V													
B.FR.11.DEMB11FR001		N	I	Y	I	H	K	NR	V													
B.HT.05.05HT_129389		A				K	K	I	NN	V												
B.JP.12.DEMB12JP001		NA				I	K	KR	V													
B.KR.07.HP_18_07JHS10_3909		N				I	K	KE	V	SN												
B.RU.11.1RU211		N				I	H	K	S	V	K	RN										
B.SE.12.SEG00057		N				I	R	R	V	K	RN											
B.TH.10.DEMB10TH002		K	H			I	H	K	Q	I	NT	K	I	E	K	K						
B.US.16.2609		N				Y	I	H	K	KS	S	T	N	V								
C.BR.11.DEMC11BR035		L				I	R	S	Y	R	V	V	E	K	OP	N	H	LR	N	G	MH	A
C.CN.10.YNFI19		L				K	N			D	R	KV										
C.DE.10.622166		L				I	I	I	R	A	RN	KV	X	RE	K	I	K	Q	H	C	SLRD	G
C.EC.14.ARP1198		K	GL			K	N			S												
C.ET.08.ET104		GL				K	N			RR	S	R	KV	X	RE	K	I	K	Q	H	C	SLRD
C.IN.15.NIRT008		L				K	N			RR	S	R	KV	X	RE	K	I	K	Q	H	C	SLRD
C.MW.09.703010256_CH256.w96		L				K	N			RR	S	R	KV	X	RE	K	I	K	Q	H	C	SLRD
C.NG.10.10NG602523		L				K	N			RR	S	R	KV	X	RE	K	I	K	Q	H	C	SLRD
C.NP.11.1NP01		L				K	N			RR	S	R	KV	X	RE	K	I	K	Q	H	C	SLRD
C.PK.14.DEMC14PK009		L				K	N			RR	S	R	KV	X	RE	K	I	K	Q	H	C	SLRD
C.SE.13.SEG00311		L				K	N			RR	S	R	KV	X	RE	K	I	K	Q	H	C	SLRD
C.TZ.08.707010457_CH457.w8		L				I	K	N	Y	R	KV											
C.US.11.17T84_4G8		L				K	K	H		RR	N	Y	R	KV								
C.ZA.13.DEMC13ZA152		L				K	K	H		RR	N	Y	R	KV								
C.ZM.11.DEMC11ZM006		GL				I	R	S	Y	R	V	V	E	K	OP	N	H	LR	N	G	MH	A
D.BR.10.10BR_R1108		D				S	Y	H	K	KR	I	K	D	K	S	VK						
D.CD.03.LA17Mu0		V				I	K	TA	D	K	K	VI										
D.CM.10.DEMD10CM009		V				Y	K	K	A	DNH	K											
D.CY.06.CY163		N				Y	K	K	A	DNH	K											
D.KE.11.DEMD11KE003		N				Y	K	K	A	DNH	K											
D.KR.04.04KR08		N				Y	K	K	A	DNH	K											
D.Z.01.Z88		N				Y	K	K	A	DNH	K											
D.UG.10.DEMD10UG004		N				Y	K	K	A	DNH	K											
D.UG.11.DEMD11UG003		N				Y	K	K	A	DNH	K											
D.YE.02.02YE516		N				Y	K	K	A	DNH	K											
F1.A0.06.A0_06_ANG32		N				Y	I	H	K	K	V	F	R	V	RR	DK	N	E	LR	G	I	SM
F1.AR.02.ARE933		N				Y	I	H	K	K	V	F	R	V	RR	DK	N	E	LR	G	I	SM
F1.BR.10.10BR_RJ015		X				Y	H	K	K	C	F	RN	V	SE	K	I	V					
F1.FR.11.DEMF11FR037		N				Y	I	N	K	C	F	RN	V	SE	K	I	V					
F1.CY.08.CY222		N				Y	H	K	KN	F	R	K	I	E	I	V						
F1.ES.02.ES_X845_4		N				Y	H	K	KN	F	R	K	I	E	I	V						
F1.ES.11.VA0053_nfl		N				Y	H	K	KN	F	R	K	I	E	I	V						
F1.FR.04.LA221_re		N				Y	H	K	KN	F	R	K	I	E	I	V						
F1.R0.03.LA20DUC1		K				S	Y	H	K	KS	F	R	V	EE	K	V						
F1.RU.08.D88_845		N				Y	H	K	K	S	F	R	V	EE	K	V						
F2.CM.02.02CM_0016BBY		N				R	K	K														
F2.CM.10.DEMF210CM007		L				R	K	K														
F2.CM.11.DEURF11CM026		N				R	K	KN	R	KV												
G.CD.03.LA23L1ed		N				I	K	GK	R	KV												
G.CM.08.709_10		V				K	K	KK	R	KV												
G.CM.10.DEMG10CM008		N				K	K	KK	R	KV												
G.CM.10.DEURF10CM020		N				I	R	K														
G.CN.08.GX_2084_08		N				K	K	KK	R	KV												
G.EC.14.ARP1201		K	A	N		I	K	K	R	KV												
G.GH.03.03GH1756		N				I	K	K	R	KV												
G.GW.08.LA57Lm0		N				I	K	K	R	KV												
G.KE.09.DEMG09KE001		N				K	K	Y	F	R	KV											
G.NG.12.12NG060409		N				K	K	Y	F	R	KV											
H.CD.04.LA19KoSa		D				NA																
H.CF.02.LA25LeM1		N				Y	K	K	OK	F	T	K	V									
H.GB.00.00GBAC4001		N																				

B. FR. 83. HXB2
02 AG. KR. 12. 12MHI11 10746
02 AG. KR. 12. 12MHR9
02 AG. LR. x. POC44951
02 AG. NG. 12. 12NG066418
02 AG. NG. x. 1BNS
02 AG. SE. x. 1E6Q2024
02 AG. SN. 13. 9580
03 AB. RU. 97. KAL153 2
04 cpx. CY. 94. 94CY032 3
95 DF. BE. x. VT110
06 cpx. AU. 96. BFP90
07 BC. CN. 98. 98CN009
08 BC. CN. 97. 97CNGX 6F
09 cpx. GH. 96. 96GH2911
10 CD. TZ. 96. 96TZ BF061
11 cpx. CM. 95. 95CM 1816
12 BF. AR. 99. ARMA159
13 cpx. CM. 96. 96CM 1849
14 BG. ES. 05. X1870
15 01B. TH. 99. 99TH MU2079
16 AZD. FR. 97. 97FR000
17 BF. AR. 99. ARMA038
18 cpx. CU. 99. CU76
19 cpx. CU. 99. CU7
20 BG. CU. 99. CU103
21 AZD. FR. 02. 02CD MBT047
22 01A1. CM. 01. 01CM 0001BBY
23 BG. CU. 03. CB118
24 BG. ES. 08. X2456 2
25 cpx. CM. 02. 1918E
26 AU. CD. 02. 02CD MBT047
27 cpx. FR. 02. 02FR K25
28 BF. BR. 99. BREPM12609
29 BF. BR. 01. BREPM16704
31 BC. BR. 04. 04BR142
32 06A1. EE. 01. E06369
33 01B. ID. 07. 07IDT189 C
34 01B. TH. 99. 99TH 1969P
35 AD. AF. 07. 169H
36 cpx. CM. 00. 00CMNYU830
37 cpx. CM. 00. 00CMNYU926
38 BF1. UY. 03. UY03 3389
39 BF. BR. 04. 04BR3179
40 BF. BR. 05. 05BRR1055
42 BF. LU. 03. luBF 01 03
43 02G. SA. 03. J11223
44 BF. CL. 08. CH80
45 cpx. FR. 04. 04FR AUK
46 BF. BR. 07. 07BR FPS625
47 BF. ES. 08. P1942
48 01B. MY. 07. 07MYKT021
49 cpx. GM. 03. N2677
50 A1D. GB. 10. 1256 GM021
51 A1D. SG. 10. 1256 GM021
52 01B. MY. 03. 03MYKL018 1
53 01B. MY. 11. 11FIR164
54 01B. MY. 09. 09MYSB023
55 01B. CN. 10. HNC5102056
56 cpx. FR. 10. 10FR patient\_A
57 BC. CN. 09. 09YNLX1959
58 01B. MY. 09. 09MYPR37
59 01B. CN. 09. 09LNA423
60 BC. IT. 11. BAV499
61 BC. CN. 10. J1100010
62 BC. CN. 10. YNFL13
63 02A1. RU. 10. 10RU6637
64 BC. CN. 09. YNFL31
65 cpx. CN. 10. YNFL01
67 01B. CN. 11. ANHUI HF115
68 01B. CN. 11. ANHUI WH73
69 01B. JP. 05. 05JPMYC113SP420
70 BF1. BR. 10. 10BR PE004
71 BF1. BR. 10. 10BR PE008
72 BF1. BR. 10. 10BR MG002
73 06. DE. 01. 01D95 01
74 01B. MY. 10. 10MYPR268
78 cpx. CN. 13. YNCT19
85 BC. CN. 14. 14CN SCYB2
86 BC. CN. 13. 13YNHS18
87 cpx. CN. 12. DH32
88 BC. CN. 05. 05YNLX2559
0. CM. 96. LA51YBF35
0. CM. 96. LA52YBF39
0. CM. 99. 99CMU4122
0. CM. x. pcM02 3
0. ES. 01. Rea025 HIV Group0
0. FR. 06. LA55RBF206
0. GA. 11. 11Gab6352
0. SN. 99. 99SE MP1299
0. SN. 99. 99SE MP1390
0. US. 10. LTNP
N. CM. 06. U14296
N. FR. 11. 11. FR 2011
P. CM. 06. U14788
P. FR. 09. RBF168
CPZ. TZ. 06. TAN5
CPZ. US. 85. US Marilyn
GOR. CM. 12. SIVgor\_B01D2
GOR. CM. 13. SIVgor\_BP1D5

Vif start
MENRWQVMIVWQVDMRIRTKWSLVKHHMYVSGKARGWYFRHHYSEPHRISSEVHPILDG. AR. LVITTYWGLHTGERDWHLGQGVSIIEWRKKRYSTQVDPELADQLIHLHYDFCDSDAIRKALLGHIVSPRCEYQAG. HN. KVGLSQLYLAALAI. . . . T. PKKIKP

Table with 3 columns: Accession ID, Amino Acid Sequence, and Reference ID. The table lists various HIV-1 protein sequences and their corresponding reference identifiers.

		Vif end	
B.FR.83.HXB2	PLPSVTKLTEDRWNKPKQTKGHRGSHTMNGH.....*		192
A1.CM.08.886.24	---K-----R-RD-----C.....		193
A1.CY.08.CY236	---K-----R-D-----C.....		193
A1.KE.11.DEMA111KE002	---R-----R-R-----C.....		193
A1.NG.10.10NG040248	---R-----R-P-N-----C.....		193
A1.PK.14.DEMA114PK001	---R-----R-P-N-----C.....		193
A1.RW.11.DEMA111RW002	---R-A-----R-P-N-I-----C.....		193
A1.UG.11.DEMA110UG009	---R-----S-----R-P-N-----C.....		193
A1.ZA.04.503.15344.T10_A1	---R-----R-P-N-----C.....		193
A2.CM.01.01CM.1445MV	---R-V-----R-N-----C.....		193
A3.SN.01.DDI579	---R-----R-----C.....		193
A4.CD.97.97CD.KCC2	---R-----R-----C.....		193
A6.BY.13.PV85	---R-----DR-N-S-C.....		193
A6.CY.09.CY255	---R-----R-R-N-----C.....		193
A6.RU.11.11RU6950	---R-----R-R-N-----C.....		193
A6.UA.12.DEMA112UA014	---R-----R-R-N-----C.....		193
B.BR.10.10BR.R1032	---R-----E-S-----C.....		193
B.CA.07.502.1191.03	---R-----I-----C.....		193
B.CH.08.M2.0803101.NFLG8	---K-----V-----C.....		189
B.CN.12.DEMB12CN006	---K-----I-----C.....		193
B.CU.14.14CU005	-V-A-----S-D-K-N-S.....		193
B.DE.13.366396	---A-----E-----C.....		193
B.ES.14.ARP1195	---K-----D-SI-----C.....		191
B.FR.11.DEMB11FR001	---K-----V-----Q-----C.....		193
B.HT.05.05HT.129389	---Q-----I-E-P-----C.....		193
B.JP.12.DEMB12JP001	---R-----E-----C.....		194
B.KR.07.HP.18.07JHS10.3909	---R-----R-D-IS-----C.....		193
B.RU.11.11RU21n	---R-----D-IS-----C.....		193
B.SE.12.SE600057	---R-----M-K-----C.....		193
B.TH.10.DEMB10TH002	---K-----S-----C.....		193
B.US.16.2609	---R-V-----R-IRDR-N-L-----C.....		193
C.BR.11.DEMC11BR035	---R-V-----N-M-R-N-----C.....		194
C.CN.10.YNFL19	---R-V-----RDR-N-----C.....		193
C.DE.10.622166	---R-A-K-----R-R-X-----C.....		193
C.ES.14.ARP1198	---S-V-K-----R-R-N-----C.....		193
C.ET.08.ET104	---I-Q-----N-R-R-----C.....		193
C.IN.15.NIRT008	---S-V-K-----R-R-N-----C.....		193
C.MW.09.703010256.CH256.w96	---R-V-----N-R-R-N-----C.....		193
C.NG.10.10NG020523	---N-Q-----V-N-----C.....		193
C.NP.11.11NP016	---S-V-----RIR-R-N-----C.....		193
C.PK.14.DEMC14PK009	---S-V-K-----R-----C.....		193
C.SE.13.SE600311	---R-V-----R-R-N-I-----C.....		193
C.TZ.08.707010457.CH457.w8	---S-V-K-----RDR-N-----C.....		193
C.US.11.17TB4.4G8	---R-V-----R-N-----C.....		193
C.ZA.13.DEMC13ZA152	---R-V-----R-N-----L-----C.....		193
C.ZM.11.DEMC11ZM006	---R-----R-----C.....		193
D.BR.10.10BR.R1108	---R-----Q-----N-----C.....		193
D.CD.03.LA17MuBo	---R-----Q-----T-----C.....		193
D.CM.10.DEMD10CM009	---R-----Q-K-E-S-----C.....		193
D.CY.06.CY163	---K-----R-E-----C.....		193
D.KE.11.DEMD11KE003	---K-----R-E-P-----WSF-----C.....		196
D.KR.04.04KR08	---K-----R-P-----C.....		193
D.TZ.01.288	---R-----R-----C.....		193
D.UG.10.DEMD10UG004	---K-----R-R-----S-----C.....		193
D.UG.11.DEMD11UG003	---K-----O-----C.....		193
D.YE.02.02YE516	---R-V-----E-----C.....		193
F1.A0.06.A0.06.ANG32	---Q-V-----R-#-D-WNFWRSL-----C.....		193
F1.AR.02.ARE933	---Q-V-----R-----C.....		199
F1.BR.10.10BR.RJ015	---Q-V-----RDR-----C.....		193
F1.FR.11.DEMF11BR037	---I-K-V-----E-R-N-----C.....		193
F1.CY.08.CY222	---R-V-----E-R-E-Y-----C.....		193
F1.ES.02.ES.X845.4	---R-V-----E-R-E-Y-----C.....		193
F1.ES.11.VA0053.nfl	---K-V-----R-P-----C.....		193
F1.FR.04.LA22LeRe	---K-V-----REIR-----C.....		194
F1.R0.03.LA20DuC1	---K-V-----E-----C.....		193
F1.RU.08.D88.845	---K-V-K-N-----C.....		194
F2.CM.02.02CM.0016BBY	---R-V-----N-R-----C.....		194
F2.CM.10.DEMF210CM007	---K-V-----N-R-----C.....		194
F2.CM.11.DEURF11CM026	---K-----R-E-P-----C.....		193
G.CD.03.LA23LiEd	---Q-----S-IR-KE-P-S-----C.....		193
G.CM.08.709.10	---K-----S-IR-KE-P-S-----C.....		193
G.CM.10.DEMG10CM008	---K-----ENP-S-----C.....		193
G.CM.10.DEURF10CM020	---K-----NPS-S-----C.....		193
G.CN.08.GX.2084.08	---R-N-----R-ENP-WNC-----C.....		196
G.ES.14.ARP1201	---R-----S-IR-R-ENL-T-----C.....		193
G.GH.03.03GH175G	---R-----ENP-S-PWKC-----C.....		196
G.GW.08.LAS7LmNe	---A-----E-----I-----C.....		193
G.KE.09.DEMG09KE001	---S-----H-R-E-S-----C.....		193
G.NG.12.12NG060409	---R-----R-----C.....		193
H.CD.04.LA19KoSa	---Q-V-----NS-R-----S-----C.....		193
H.CF.02.LA25LeM1	---Q-V-----T-E-----C.....		193
H.GB.00.00GBAC4001	---V-Q-V-----R-----S-Q-----C.....		193
J.CD.03.LA26D1An	---V-K-V-----R-Q-----C.....		193
J.CD.97.J.97DC.KTB147	---K-----G-GENP-----C.....		192
J.SE.93.SE9280.7887	---R-----R-ENP-S-WNC-----C.....		196
K.CD.97.97ZR.EQTB11	---K-----IR-ENPS-----C.....		193
K.CM.96.96CM.MP535	---K-----SE-R-ENP-----C.....		193
01.AE.AF.07.569M	---K-----I-ENL-----C.....		193
01.AE.CM.11.1156.26	---K-----IR-P-----C.....		189
01.AE.CN.12.DE00112CN011	---K-----R-DNP-----C.....		193
01.AE.HK.04.HK001	---K-----IRA-ENP-----C.....		193
01.AE.IR.10.10IR.THR48F	---E-I-----R-ENP-----C.....		191
01.AE.JP.11.DE00111JP003	---K-----KE-IR-ENS-----C.....		193
01.AE.SE.11.SE601018	---R-A-A-----KE-IRD-S-----C.....		193
01.AE.TH.10.DE00110TH001	---K-----E-----RS-----C.....		193
01.AE.TH.90.CM240			193
01.AE.US.05.306163.FL			191
02.AG.CM.10.DE0010CM013			193
02.AG.DE.08.701114			193
02.AG.GW.05.CC.0048			193





Vpr start	amphipathic $\alpha$ -helix oligomerization		H(S/N)RIG motifs		Vpr end
			Vpr end in HXB2	frameshift in HXB2	
B. FR. 83. HXB2	MEQAPEDQGPQREPHEWTLLELLEELKNEAVRHFRPIRV.LHGLGQHIYETYGDVTWAGVEAIRILQQLLFTH.#FRIGRCHSRIGV.T...R.QRRA...RNGASRS*				
02 AG. KR. 12. 12MHI11 10746	-RP	F-M-H-P	Y-E-V-0-I-I	G-G-G-G	G
02 AG. KR. 12. 12MHR9	-R	V-P	N-N-G-T-H-V-0-I-I	G-G-G-G	G
02 AG. LR. x. POC44951	-	Q-P	Y-N-EY-N-T-V-0-I-I	G-G-G-G	S
02 AG. NG. 12. 12NG066418	-R	H-P	Q-V-V-0-I-I	G-G-G-G	G
02 AG. NG. x. IBN0	-	H-P	E-Q-N-E-G-V-0-I-I	P-G-G-G	S
02 AG. SE. x. E6G02024	-R	H-P	Q-V-V-0-I-I	P-G-G-G	S
02 AG. SN. 13. 9580	-R	H-P	Q-V-V-0-I-I	P-G-G-G	SG
03 AB. RU. 97. KAL153 2		S-V	S-Y-N-E-N-0-I-I	Q-R	
04 cpx. CY. 94. 94CY032 3		I-P	Y-N-N-E-V-0-I-I	P-R.#AGD	
05 DF. BE. x. VT110		I-P	Y-N-N-E-V-0-I-I	P-R.#AGD	S
06 cpx. AU. 96. BFP90		S-P	NI-Y-S-E-LL-T-L-V-H-I-L	P-G-G-G	
07 BC. CN. 98. 98CN009		Y-P	Y-N-N-E-V-0-I-I	P-G-G-G	
08 BC. CN. 97. 97CNG 6F		Q-P	YV-T-T-L-T	I-V	
09 cpx. GH. 96. 96GH2911		N-P	D-T-V-H-I-I	GR-G-D-G	
10 CD. TZ. 96. 96TZ BF061		Y-P	N-N-V-V-0-I-I	P-G-G-G	T-T
11 cpx. CM. 95. 95CM 1816		M-H-P	N-N-V-V-0-I-I	P-G-G-G	
12 BF. AR. 99. ARMA159		P-P	N-N-V-V-0-I-I	P-G-G-G	
13 cpx. CM. 96. 96CM 1849		N-H-K-P	N-N-V-V-0-I-I	P-G-G-G	S
14 BG. ES. 05. X1870		N-P	N-N-V-V-0-I-I	P-G-G-G	
15 01B. TH. 99. 99TH MU2079	G	Y-G-P-D-R-K-S-P	Y-N-S-TN-V-H-V-H-AI-I	P-G-G-R-PG	
16 AZD. KR. 97. 97KR008		Y-P	Y-N-N-E-V-0-I-I	P-G-G-G	
17 BF. AR. 99. ARMA038	G	Y-P	Y-N-N-E-V-0-I-I	P-G-G-G	
18 cpx. CU. 99. CU76		N-P	Y-N-N-E-V-0-I-I	P-G-G-G	
19 cpx. CU. 99. CU7		N-Y-A-D-P	YV-T-E-N-E-V-0-I-I	P-R-V-D-PG	
20 BG. CU. 99. CU103		D-P	Y-N-N-E-V-0-I-I	P-G-G-G	
21 AZD. KE. 99. KER2003		D-P	Y-N-N-E-V-0-I-I	P-G-G-G	
22 01A1. CM. 01. 011CM 0001BBY		V-Y-V-S-GP	E-N-N-E-V-0-I-I	P-G-G-G	S
23 BG. CU. 03. CB118		Q-P	V-N-N-E-V-0-I-I	P-R-G-PG	
24 BG. ES. 08. X2456 2		N-P	N-N-V-V-0-I-I	P-R-R-D-SG	
25 cpx. CM. 02. 19181E		N-P	N-N-V-V-0-I-I	P-G-G-G	
26 AU. CD. 02. 02CD MBT047		Y-I-Q-P	Y-N-N-E-V-0-I-I	P-S-G-G	P-P
27 cpx. FR. 04. 04CD FR K25		Y-P	Y-N-N-E-V-0-I-I	P-G-G-G	
28 BF. BR. 99. BREPM12609		Y-S-P	Y-N-N-E-V-0-I-I	P-G-G-G	
29 BF. BR. 01. BREPM16704		Y-S-P	Y-N-N-E-V-0-I-I	P-G-G-G	
31 BC. BR. 04. 04BR142		N-P	Y-N-N-E-V-0-I-I	P-G-G-G	
32 06A1. EE. 01. EE0369	-R	N-S-K-P	Y-N-N-E-V-0-I-I	P-G-G-G	S
33 01B. ID. 07. JKT189 C		Y-P	Y-N-N-E-V-0-I-I	P-G-G-G	
34 01B. TH. 99. 01B1969P	A	Y-P	Y-N-N-E-V-0-I-I	P-G-G-G	
35 AD. AF. 07. 169H		Y-M-D-H-P	Q-Y-N-E-V-0-I-I	P-G-G-G	D-SG-P
36 cpx. CM. 00. 00CMNYU830		F-A-H-P	Y-N-N-E-V-0-I-I	P-G-G-G	
37 cpx. CM. 00. 00CMNYU926		Y-A-P	Y-N-N-E-V-0-I-I	P-R-V-P	
38 BF1. UY. 03. UY03 3389		Y-T-P	S-Y-N-E-V-0-I-I	P-G-G-G	
39 BF. BR. 04. 04BR3179	H	Y-T-P	S-Y-N-E-V-0-I-I	P-G-G-G	
40 BF. BR. 05. 05BRRJ055		Y-S-P	N-Y-I-T-I-T	I-I	
42 BF. LU. 03. luBF 01 03		Y-P	N-Y-I-T-I-T	I-I	
43 02G. SA. 03. J11223	V	X-H-S-P	Y-N-N-E-V-0-I-I	P-G-G-G	H-G
44 BF. CL. 00. CH80	G	Y-S-P	Y-N-N-E-V-0-I-I	P-G-G-G	N
45 cpx. FR. 04. 04FR AUK		Y-M-P	Y-N-N-E-V-0-I-I	P-G-G-G	D-PG
46 BF. BR. 07. 07BR FPS625	G	Y-P	Y-N-N-E-V-0-I-I	P-G-G-G	
47 BF. ES. 08. P1942		Y-P	Y-N-N-E-V-0-I-I	P-G-G-G	
48 01B. MY. 07. 07MYKT021		Y-P	Y-N-N-E-V-0-I-I	P-G-G-G	R
49 cpx. GM. 03. N26677		Y-P	Y-N-N-E-V-0-I-I	P-G-G-G	
50 A10. GB. 10. 12752	-R	Y-Q-A-DM-D-H	Y-N-N-E-V-0-I-I	P-G-G-G	S-P
51 01B. SG. 11. 11792 HM021		Y-P	Y-N-N-E-V-0-I-I	P-G-G-G	
52 01B. MY. 03. 03MYKL018 1		A-Y-A-P	Y-Y-TN-V-0-I-I	P-G-G-G	P
53 01B. MY. 11. 11FIR164		H-P	X-N-N-E-Q-V-0-I-I	P-G-G-G	
54 01B. MY. 09. 09MYSB023		S-P	L-X-N-RE-V-0-I-I	P-G-G-G	G
55 01B. CN. 10. HNC5102056	H	Y-P	N-N-E-V-0-I-I	P-G-G-G	G
56 cpx. FR. 10. URFS patient A		S-H-P	N-N-E-V-0-I-I	P-G-G-G	D-SD
57 BC. CN. 09. 09NLY195g	P	S-P	YV-T-K-V-0-I-I	P-G-G-G	
58 01B. MY. 09. 09MYPR37		T-P	Y-N-N-E-V-0-I-I	P-G-G-G	
59 01B. CN. 09. 09LNA423	H	Y-A-P	Y-H-T-V-0-I-I	P-G-G-G	G
60 BC. IT. 11. BAV499		Y-A-Q-P	Y-N-N-E-V-0-I-I	P-G-G-G	N
61 BC. CN. 10. J1100010		P-P	YV-DN-T-V-0-I-I	P-G-G-G	
62 BC. CN. 10. YNFL13	P	YX-Q-T-P	Y-N-N-E-V-0-I-I	P-G-G-G	
63 02A1. RU. 10. 10RU6637		F-H-P	Y-N-N-E-V-0-I-I	P-G-G-G	S
64 BC. CN. 09. YNFL31	-RP	H-Y-Q-P	YV-N-T-T-V-0-I-I	P-G-G-G	
65 cpx. CN. 10. YNFL01		R-G-Q-P	Y-N-N-E-V-0-I-I	P-G-G-G	
67 01B. CN. 11. ANHUI HF115	N	Y-A-P	Y-N-N-E-V-0-I-I	P-G-G-G	G
68 01B. CN. 11. ANHUI WH73		Y-A-P	Y-N-N-E-V-0-I-I	P-G-G-G	
69 01B. JP. 05. 05JPMYC113SP420		Y-A-A-P	Y-N-N-E-V-0-I-I	P-G-G-G	G
70 BF1. BR. 10. 10BR PE004		Y-A-S-P	Y-N-N-E-V-0-I-I	P-G-G-G	TG
71 BF1. BR. 10. 10BR PE008		Y-P	Y-N-N-E-V-0-I-I	P-G-G-G	G
72 BF1. BR. 10. 10BR MG002	-R	Y-P	Y-N-N-E-V-0-I-I	P-G-G-G	
73 BG. DE. 01. 9196 01		A-Y-A-S-P	Y-N-N-E-V-0-I-I	P-G-G-G	PG
74 01B. MY. 10. 10MYPR268		Y-A-S-P	Y-N-N-E-V-0-I-I	P-G-G-G	TG
78 cpx. CN. 13. YNTC19		Y-A-P	Y-N-N-E-V-0-I-I	P-G-G-G	PG
85 BC. CN. 14. 14CN SCYB2	P	F-A-O-P	YV-D-H-I-V-I	P-G-G-G	
86 BC. CN. 13. 13YHNS18	P	Y-Q-AI-Q-P	LY-S-V-V-0-I-I	P-G-G-G	P
87 cpx. CN. 12. DH32		Y-Q-P	Y-V-V-0-I-I	P-G-G-G	
88 BC. CN. 05. 05YNRL25sg	H	Y-A-Q-P	YV-D-T-T-V-0-I-I	P-G-G-G	
0. CM. 96. LA51YBF35		A-F-A-A-N	QA-Y-D-E-M-A-0-I-I	NPSNP-R-GR-D-S	
0. CM. 96. LA52YBF39	V	A-F-A-A-N	QA-Y-D-E-M-A-0-I-I	NPSNP-R-GR-D-S	
0. CM. 99. 99CMU4122	H	A-F-A-T-D-A-P	A-Y-V-I-M-T-0-I-I	NPSNT-G-GR-S	
0. CM. x. pCM02 3		P-F-A-T-D-A-P	A-Y-V-I-M-T-0-I-I	NPSNT-G-GR-S	
0. ES. 01. Rea025 HIV Group0		P-F-A-T-D-A-P	A-Y-V-I-M-T-0-I-I	NPSNT-G-GR-S	
0. FR. 06. LA55RBF206	N	V-V-A-A-N	QA-Y-D-E-G-I-A-0-I-I	NPSST-G-GR-S	
0. GA. 11. 11GAb6352	N	P-F-A-A-P	A-Y-V-M-T-0-I-I	NPTNP-G-GR-S	
0. SN. 99. 99SE MP1299		A-F-S-A-P	QA-Y-D-V-M-H-A-0-I-I	PSNT-G-GR-S	
0. SN. 99. 99SE MP1300		A-F-S-A-P	QA-Y-D-V-M-H-A-0-I-I	PSNT-G-GR-S	
0. US. 10. LTNP		A-F-A-T-H-P	Y-N-R-M-M-T-Y-0-I-I	P-G-G-G	
N. CM. 06. UI4206	-R	A-Y-A-P	N-N-E-V-0-I-I	P-G-G-G	
N. FR. 11. N1 FR 2011	-R	T-Y-A-P	N-N-E-V-0-I-I	P-G-G-G	I
P. CM. 06. UI4788	P	P-F-M-OT-E	S-Y-N-E-T-I	LTP-S-R-GR-H-P	
P. FR. 09. RBF168	P	F-M-OT-A-P	LOY-S-Y-N-E-T-I	LTP-S-R-GR-H-P	
CPZ. TZ. 06. TAN5		YTL-L-DT-I-Q	TV-Q-V-NWVFTVH-S-E	QEL-RA-T-Y-H-A-S	
CPZ. US. 85. US Marilyn	V	A-Y-A-DV-E-L	P-Q-Y-S-E	Y-N-I-S-L-A-TPQGR-S	
GOR. CM. 12. SIVgor_B0ID2	V	A-F-A-V-A-LK	P-A-Y-D-V-M-H-A-0-I-I	IPNSA-G-R-P	
GOR. CM. 13. SIVgor_BPID15	R	P-F-M-T-A-P	S-D-E-T-I-Y-P	IPNSA-G-R-H-PN	





	Rev start	exon 1 end	exon 2 start	NLS	Leu-rich effector domain	Rev end
B.FR.83.HXB2	MAGRS	SD	.E	ELIRT	VRLIKL.....LYQSNPP.PN.PE.GTRQARRNRWRERQRQIHISERILGTYLGRSAEPVLPQLPPLERLTLDCNEDCGTSGTQ.....GVGSPQILVESPTVL.ESG	TKK...G
A1.CM.08.886.24						
A1.CY.08.CY236						
A1.KE.11.DEMA111KE002						
A1.NG.10.10NG040248						
A1.PK.14.DEMA114PK001						
A1.RW.11.DEMA111RW002						
A1.UG.11.DEMA110UG009						
A1.ZA.04.503.15344.T10_A1						
A2.CM.01.01CM.1445MV						
A3.SN.01.DD1579						
A4.CD.97.97CD.KCC2						
A6.BY.13.PV85						
A6.CY.09.CY255						
A6.RU.11.11RU06950						
A6.UA.12.DEMA112UA014						
B.BR.10.10BR.R1032						
B.CA.07.502.1191.03						
B.CH.08.M2.0803101.NFLG8						
B.CN.12.DEMB12CN006						
B.CU.14.14CU005						
B.DE.13.366396						
B.ES.14.ARP1195						
B.FR.11.DEMB11FR001						
B.HT.05.05HT.129389						
B.JP.12.DEMB12JP001						
B.KR.07.HP.18.07JHS10.3909						
B.RU.11.11RU21n						
B.SE.12.SE600057						
B.TH.10.DEMB10TH002						
B.US.16.2609						
C.BR.11.DEMC11BR035						
C.CN.10.YNFI19						
C.DE.10.622166						
C.ES.14.ARP1198						
C.ET.08.ET104						
C.IN.15.NIRT008						
C.MW.09.703010256.CH256.w96						
C.NG.10.10NG0820523						
C.NP.11.11NP016						
C.PK.14.DEMC14PK009						
C.SE.13.SE600311						
C.TZ.08.707010457.CH457.w8						
C.US.11.17T84.4G8						
C.ZA.13.DEMC13ZA152						
C.ZM.11.DEMC11ZM006						
D.BR.10.10BR.R1108						
D.CD.03.LA17MuBo						
D.CM.10.DEMD10CM009						
D.CY.06.CY163						
D.KE.11.DEMD11KE003						
D.KR.04.04KR08						
D.TZ.01.288						
D.UG.10.DEMD10UG004						
D.UG.11.DEMD11UG003						
D.YE.02.02YE516						
F1.A0.06.A0.06.ANG32						
F1.AR.02.ARE933						
F1.BR.10.10BR.RJ015						
F1.BR.11.DEMF11BR037						
F1.CY.08.CY222						
F1.ES.02.ES.X845.4						
F1.ES.11.VA0053.nf1						
F1.FR.04.LA221eRe						
F1.RO.03.LA20DUC1						
F1.RU.08.D88.845						
F2.CM.02.02CM.0016BBY						
F2.CM.10.DEMF210CM007						
F2.CM.11.DEURF11CM026						
G.CD.03.LA23L1Ed						
G.CM.08.709.10						
G.CM.10.DEMG10CM008						
G.CM.10.DEURF10CM020						
G.CN.08.GX.2084.08						
G.ES.14.ARP1201						
G.GH.03.03GH175G						
G.GW.08.LAS7MnE						
G.KE.09.DEMG09KE001						
G.NG.12.12NG060409						
H.CD.04.LA19KoS						
H.CF.02.LA25LeM1						
H.GB.00.00GBAC4001						
J.CD.03.LA26D1An						
J.CD.07.1.970C.KTB147						
J.SE.93.5E9280.7887						
K.CD.97.97ZR.E0T811						
K.CM.96.96CM.MP535						
01.AE.AF.07.569M						
01.AE.CM.11.1156.26						
01.AE.CN.12.DE00112CN011						
01.AE.HK.04.HK001						
01.AE.IR.10.10IR.THR48F						
01.AE.JP.11.DE00111JP003						
01.AE.SE.11.SE601018						
01.AE.TH.10.DE00110TH001						
01.AE.TH.90.CM240						
01.AE.US.05.306163.FL						
02.AG.CM.10.DE00210CM013						
02.AG.DE.07.081114						
02.AG.GW.05.CC.0048						

B.FR.83.HXB2
02 AG.KR.12.12MHI11 10746
02 AG.KR.12.12MHR9
02 AG.LR.x.POC44951
02 AG.NG.12.12NG060418
02 AG.NG.x.IBNG
02 AG.SG.05.E6G02024
02 AG.SN.13.9580
03 AB.RU.97.KAL153 2
04 cpx.CY.94.94CY032 3
05 DF.BE.x.VT110
06 cpx.AU.96.BFP90
07 BC.CN.98.98CN009
08 BC.CN.97.97CN6X 6F
09 cpx.GH.96.96GH2911
10 CD.TZ.96.96TZ BF061
11 cpx.CM.95.95CM 1816
12 BF.AR.99.ARMA159
13 cpx.CM.96.96CM 1849
14 BG.ES.05.X1870
15 01B.TH.99.99TH MU2079
16 AZD.FR.97.97KR00
17 BF.AR.99.ARMA038
18 cpx.CU.99.CU76
19 cpx.CU.99.CU7
20 BG.CU.99.CU103
21 AZD.FR.97.97KR00
22 02A1.CM.01.01CM 0001BBY
23 BG.CU.03.CB118
24 BG.ES.08.X2456 2
25 cpx.CM.02.19181E
26 AU.CD.02.02CD MBT047
27 cpx.FR.04.04CD FR K25
28 BF.BR.99.BREPM12609
29 BF.BR.01.BREPM16704
31 BC.BR.04.04BR142
32 06A1.EE.01.EE0369
33 01B.ID.07.07JKT189 C
34 01B.TH.99.09TR1969P
35 AD.AF.07.169H
36 cpx.CM.00.00CMNYU830
37 cpx.CM.00.00CMNYU926
38 BF1.UY.03.UY03 3389
39 BF.BR.04.04BR13179
40 BF.BR.05.05BRR1055
42 BF.LU.03.LuBF 01 03
43 02G.SA.03.J11223
44 BF.CL.00.CH80
45 cpx.FR.04.04FR AUK
46 BF.BR.07.07BR FPS625
47 BF.ES.08.P1942
48 01B.MY.07.07MYKT021
49 cpx.GM.03.N26677
50 A1D.GB.10.12702
51 01B.SG.11.11SG HM021
52 01B.MY.03.03MYKL018 1
53 01B.MY.11.11FIR164
54 01B.MY.09.09MYSB023
55 01B.CN.10.HNCS102056
56 cpx.FR.10.URF5 patient A
57 BC.CN.09.09YNLX1959
58 01B.MY.09.09MYPR37
59 01B.CN.09.09LNA423
60 BC.IT.11.BAV499
61 BC.CN.10.J1100010
62 BC.CN.10.YNFL13
63 02A1.RU.10.10RU6637
64 BC.CN.09.YNFL31
65 cpx.CN.10.YNFL01
67 01B.CN.11.ANHUI HF115
68 01B.CN.11.ANHUI WH73
69 01B.JP.05.05JPMYC113SP420
70 BF1.BR.10.10BR PE004
71 BF1.BR.10.10BR PE008
72 BF1.BR.10.10BR MG002
73 BG.DE.01.9196 01
74 01B.MY.10.10MYPR268
78 cpx.CN.13.YNCT19
85 BC.CN.14.14CN SCYB2
86 BC.CN.13.15YH518
87 cpx.CN.12.DH32
88 BC.CN.05.05YVRL259g
0.CM.96.LA51YBF35
0.CM.96.LA52YBF39
0.CM.99.99CMU4122
0.CM.x.pCM02 3
0.E5.01.Read25 HIV Group0
0.FR.06.LA55RBF206
0.GA.11.11Gab6352
0.SN.99.99SE MP1299
0.SN.99.99SE MP1300
0.US.10.LTNP
01.06.U14296
N.FR.11.N1.FR 2011
P.CM.06.U14788
P.FR.09.RBF168
CPZ.TZ.06.TAN5
CPZ.US.85.US Marilyn
GOR.CM.12.SIVgor\_BPID2
GOR.CM.13.SIVgor\_BPID15

Table with columns: Rev start, exon 1 end, exon 2 start, NLS, Leu-rich effector domain, Rev end. It contains a dense grid of amino acid sequences for various HIV-1 protein variants.

116
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	transmembrane domain	phos phosph	cytoplasmic domain		Vpu end	
	Vpu start		α-helix	α-helix		
B.FR.83.HXB2	TOPPI...P...I	VAIVALVVAIIIAIVVMSIVIIIEYRKI...	LRQRKIDRLIDRLIERAE	DSGNESE	GEISA.LV.E...M.GVEMGHAPWD.VDDL...*	
A1.CM.08.886.24	MLSLGIWE	...W...G...I...V...L...T...V...C	...K...K...-...K...I...A...I...R...	...D...DTDE	...A...R...L...-...N...Y...N...L...G...D...N...	
A1.CY.08.CY236	MT...L...E...	...S...G...-...V...S...T...T...G...I	...K...R...V...-...K...R...-...N...I...E...R...	...D...DTDE	...A...L...L...-...N...Y...D...L...G...D...N...	
A1.KE.11.DEM111KE002	MT...L...E...	...S...G...-...L...A...I...L...I...L...I	...K...R...I...K...L...-...K...R...-...N...I...E...R...	...D...DREE	...S...K...K...L...I...D...D...V...D...L...G...D...N...	
A1.NG.10.10NG040248	MI...L...V...E...	...A...I...G...-...I...A...I...I...T...A	...T...A...Y...L...-...W...K...-...N...W...Y...N...T...	...D...DTEE	...A...A...L...G...-...P...V...L...G...D...N...	
A1.PK.14.DEM114PK001	ML...L...V...E...	...C...G...I...L...L...I...T...G...L	...C...A...T...-...G...L...-...K...I...R...	...D...DTDD	...A...T...L...I...D...D...Y...D...F...G...D...N...	
A1.RW.11.DEM111RW002	M...L...L...V...E...	...V...W...I...G...I...L...L...I...T...G	...L...K...L...-...K...L...E...I...R...	...D...DTEE	...W...A...L...L...D...D...Y...D...F...G...D...N...	
A1.UG.11.DEM110UG009	MR...L...E...	...W...G...I...L...L...I...T...G...L	...K...R...L...R...K...-...E...I...K...E...	...D...DTEE	...A...G...L...L...I...N...Y...D...L...G...D...N...	
A1.ZA.04.503.15344.T10.A1	M...T...L...L...E...	...W...T...G...L...L...T...F...G...V	...K...K...-...K...K...I...S...	...D...DAEE	...S...A...L...L...-...Y...D...N...L...G...Y...I...N...	
A2.CM.01.01CM.1445MV	ML...L...A...	...L...S...G...I...F...L...T...F...O	...K...V...K...K...-...W...K...I...S...	...D...DTEE	...S...T...L...M...-...V...L...D...F...-...A...N...N...	
A3.SN.01.DD1579	M...T...S...L...E...	...W...I...G...I...L...L...T...G...K	...V...K...K...R...E...I...R...	...D...DTEE	...S...T...L...V...D...D...I...L...Y...D...N...N...	
A4.CD.97.97CD.KCC2	M...N...L...E...	...W...S...I...I...F...L...G...I...A	...F...K...L...R...K...-...W...E...I...R...	...D...DTEE	...S...T...L...M...-...N...L...D...F...L...-...N...N...N...	
A6.BY.13.PV85	M...T...L...V...E...	...C...A...-...V...S...-...I...T...G	...L...L...L...K...-...E...I...R...	...D...DEEE	...S...T...L...M...-...G...N...L...L...-...N...N...V...	
A6.CY.09.CY255	M...T...L...E...	...Y...A...-...V...F...V...A...A	...G...L...L...L...K...-...E...I...R...	...D...DAEE	...S...T...L...M...-...V...D...Y...V...L...D...N...N...V...	
A6.RU.11.11RU6950	M...T...L...E...	...Y...A...-...V...F...V...A...A	...G...L...R...L...K...-...E...I...R...	...D...DEEE	...S...T...L...M...-...N...L...L...D...N...N...V...	
A6.UA.12.DEM112UA014	ML...L...Q...	...A...X...V...A...F...-...F...-...L	...I...L...I...L...L...I...R...	...D...DEEO	...A...A...L...M...-...N...N...V...N...	
B.BR.10.10BR.R1032	M...L...A...	...A...A...L...T...G...-...N...L	...I...A...D...-...D...E...E...I...R...	...D...DOEE	...S...A...L...V...A...L...V...E...R...G...H...L...-...N...	
B.CA.07.502.1191.03	M...T...L...Y...	...W...S...-...A...-...T...A...L...R	...R...-...I...R...T...D...DOEE	...D...DOEE	...S...A...L...D...D...-...N...N...N...EC	
B.CH.08.M2.0803101.NFLG8	M...L...I...	...V...L...A...-...A...L...T...F	...L...-...R...-...I...R...T...D...DOEE	...D...DOEE	...S...A...L...D...D...-...N...N...N...EC	
B.CN.12.DEMB12CN006	M...L...V...	...G...T...A...M...F...X...-...N	...I...R...T...D...DOEE	...D...DOEE	...S...A...L...D...D...-...N...N...N...EC	
B.CU.14.14CU085	M...L...V...	...G...T...A...M...F...X...-...N	...I...R...T...D...DOEE	...D...DOEE	...S...A...L...D...D...-...N...N...N...EC	
B.DE.13.366396	M...L...V...	...G...T...A...M...F...X...-...N	...I...R...T...D...DOEE	...D...DOEE	...S...A...L...D...D...-...N...N...N...EC	
B.ES.14.ARP1195	M...L...V...	...G...T...A...M...F...X...-...N	...I...R...T...D...DOEE	...D...DOEE	...S...A...L...D...D...-...N...N...N...EC	
B.FR.11.DEMB11FR001	M...S...L...T...	...L...T...F...F...X...-...K...K...R	...I...R...T...D...DOEE	...D...DOEE	...S...A...L...M...-...L...D...-...N...N...M...	
B.HT.05.05HT.129389	M...S...L...X...	...X...L...X...I...X...F...X...K...K...R	...I...R...T...D...DOEE	...D...DOEE	...S...A...L...M...-...L...D...-...N...N...M...	
B.JP.12.DEMB12JP001	M...L...Q...	...L...A...T...G...K...K...N...S	...I...R...T...D...DOEE	...D...DOEE	...S...A...L...M...-...L...D...-...N...N...M...	
B.KR.07.HP.18.07JHS10.3909	M...S...L...T...	...L...A...T...G...K...K...N...S	...I...R...T...D...DOEE	...D...DOEE	...S...A...L...M...-...L...D...-...N...N...M...	
B.RU.11.11RU21r	M...S...L...V...	...L...A...T...G...K...K...N...S	...I...R...T...D...DOEE	...D...DOEE	...S...A...L...M...-...L...D...-...N...N...M...	
B.SE.12.SEG00057	M...S...L...V...	...L...A...T...G...K...K...N...S	...I...R...T...D...DOEE	...D...DOEE	...S...A...L...M...-...L...D...-...N...N...M...	
B.TH.10.DEMB10TH002	M...S...S...L...Y...	...L...A...T...G...K...K...N...S	...I...R...T...D...DOEE	...D...DOEE	...S...A...L...M...-...L...D...-...N...N...M...	
B.US.16.2609	M...F...S...L...K...	...L...A...T...G...K...K...N...S	...I...R...T...D...DOEE	...D...DOEE	...S...A...L...M...-...L...D...-...N...N...M...	
C.BR.11.DEMC11BR035	M...V...N...L...	...L...E...K...I...D...Y...K...I...G...V	...-...A...L...V...I...T...Y...-...L	...V...R...W...K...I...R...	...D...DTEE	...Q...T...M...D...-...L...R...L...L...-...N...N...
C.CN.10.YNFI19	M...V...D...	...L...D...Y...K...I...G...V...F...I	...-...L...L...I...T...A...Y...-...L	...T...K...W...K...I...G...I...R...	...D...DTEE	...M...D...R...L...L...L...-...G...N...
C.DE.10.622166	M...I...N...L...	...A...A...I...V...D...Y...R...I...G...V	...F...I...L...I...T...A...Y...L	...L...V...K...N...W...K...I...R...	...D...DTEE	...S...T...M...D...-...L...R...L...L...-...D...N...
C.ES.14.ARP1198	M...L...D...	...L...T...R...V...D...Y...R...I...G...V	...F...I...L...I...T...A...Y...L	...L...V...K...N...W...K...I...R...	...D...DTEE	...S...T...M...D...-...L...R...L...L...-...D...N...
C.ET.08.ET104	M...T...N...F...	...L...E...Q...V...D...Y...R...I...G...V	...F...I...L...I...T...A...Y...L	...L...V...K...N...W...K...I...R...	...D...DTEE	...S...A...M...D...-...N...L...R...L...M...-...A...V...
C.IN.15.NIRT008	M...V...D...	...L...G...Y...K...L...T...V...G...I	...-...L...L...T...Y...K...L...-...W	...E...I...R...T...D...DMED	...D...DMED	...S...T...M...D...-...N...L...R...L...L...-...N...E...
C.MW.09.703010256.CH256.w96	M...L...D...	...L...V...A...R...V...D...Y...R...I...G...V	...F...I...L...I...T...I...L...A...Y	...L...I...L...K...R...W...K...I...R...	...D...DTEE	...S...T...M...D...-...L...G...L...L...-...N...G...
C.NG.10.10NG6026523	M...L...E...	...L...D...Y...R...I...G...V...F...I	...L...I...L...I...T...I...A...Y...-...L	...V...T...W...K...I...R...	...D...DHEE	...S...T...M...D...-...Q...L...R...L...-...A...N...G...
C.NP.11.11NP016	M...L...N...	...L...E...R...V...D...Y...R...I...G...V	...F...I...L...I...T...Y...L...K...L	...V...K...-...E...I...R...	...D...DEE	...S...T...M...D...-...L...G...L...L...-...V...G...N...
C.PK.14.DEMC14PK009	M...V...D...	...L...T...A...G...V...D...Y...R...I...G	...V...F...I...L...I...T...I...Y...L	...L...V...N...N...W...K...I...R...	...D...DTEE	...S...T...M...D...-...N...L...R...L...L...-...A...V...
C.SE.13.SEG000311	M...L...D...	...L...A...R...V...D...Y...R...I...G...V	...F...I...L...I...T...L...I...L...A...Y	...L...K...R...W...K...I...R...	...D...DTDE	...A...T...M...D...-...N...L...R...L...L...-...I...N...
C.TZ.08.707010457.CH457.w8	M...L...D...	...L...A...R...V...D...Y...R...I...G...V	...F...I...L...I...T...L...I...L...A...Y	...L...K...R...W...K...I...R...	...D...DTDE	...A...T...M...D...-...N...L...R...L...L...-...I...N...
C.US.11.17T84.4G8	M...L...D...	...L...A...R...V...D...Y...R...I...G...V	...F...I...L...I...T...L...I...L...A...Y	...L...K...R...W...K...I...R...	...D...DTDE	...A...T...M...D...-...N...L...R...L...L...-...I...N...
C.ZA.13.DEMC13ZA152	M...L...N...	...L...E...R...V...D...Y...R...I...G...V	...F...I...L...I...T...Y...L...K...L	...V...K...-...E...I...R...	...D...DHEE	...S...T...M...D...-...L...R...L...L...-...N...G...N...
C.ZM.11.DEMC11ZM006	M...S...I...S...	...L...E...R...V...D...Y...R...I...G...V	...F...I...L...I...T...Y...L...K...L	...V...K...-...E...I...R...	...D...DHEE	...S...T...M...D...-...L...R...L...L...-...N...G...N...
D.BR.10.10BR.R1108	M...L...V...	...L...I...-...T...G...L...A...T...F	...-...R...-...Y...-...I...R...	...D...DTEE	...S...K...L...D...-...Q...-...V...-	
D.CD.03.LA17MuBo	M...K...L...E...	...A...-...S...L...T...Y...-...K	...K...W...I...O...-...I...R...	...D...DREE	...S...T...L...V...A...-...I...N...-	
D.CM.10.DEMD10CM009	M...L...V...	...L...I...S...T...L...T...Y...-...Q	...K...W...I...R...E...I...R...	...D...DKEE	...S...T...L...D...-...I...V...A...-	
D.CY.06.CY163	M...S...L...E...	...L...A...-...L...L...T...Y...-...K	...W...I...G...-...W...I...R...	...D...DKEE	...S...O...L...M...-...N...V...A...-...I...N...	
D.KE.11.DEMD11KE003	M...S...L...Q...	...A...-...I...S...I...L...L...V...T	...F...C...R...L...R...#...-...W...I...R...	...D...DEEE	...S...A...F...G...Y...-...I...N...I...	
D.KR.04.04KR08	M...V...T...	...L...A...T...A...-...I...S...L...T...Y	...C...R...L...R...K...K...W...I...R...	...D...DTEE	...S...T...L...M...-...N...I...N...-	
D.NZ.01.01NZ28r	M...T...L...E...	...T...A...-...I...S...L...T...Y...C	...R...K...K...W...I...R...	...D...DTEE	...S...T...L...M...-...N...I...N...-	
D.UG.10.DEMD10UG004	M...L...V...	...L...-...L...L...L...T...F...C	...L...R...K...W...I...R...	...D...DEEE	...S...K...F...M...-...N...I...M...-	
D.UG.11.DEMD11UG003	M...N...L...	...L...V...I...G...-...L...A...-...F	...W...R...L...K...K...I...N...I...A...	...D...DREE	...S...A...L...G...L...-...I...G...I...-	
D.YE.02.02YE516	M...T...L...E...	...L...S...I...A...-...I...T...Y...-...K	...R...Q...-...I...R...	...D...DEEE	...S...T...L...M...-...A...N...V...A...-	
F1.A0.06.A0.06.ANG32	M...S...D...L...	...L...A...I...-...L...-...T...A...Y	...L...-...V...V...K...R...N...Y...E...I...R...	...D...DAEE	...A...A...L...G...V...P...F...I...G...I...N...N...	
F1.AR.02.ARE933	M...S...Y...L...	...L...A...I...G...-...I...L...-...T...A	...Y...L...L...L...I...L...I...L...Y...R...N...Y...K...I...R...	...D...DAEE	...A...A...L...G...V...P...F...I...G...I...N...N...	
F1.BR.10.10BR.RJ015	M...I...S...L...	...L...A...I...S...A...I...L...V...T...F	...K...L...R...K...-...N...Y...E...R...-	...D...DAEE	...A...A...L...G...V...P...F...I...G...I...N...N...	
F1.BF.11.DEMF11BR037	M...I...S...L...	...L...A...I...S...A...I...L...V...T...F	...K...L...R...K...-...N...Y...E...R...-	...D...DAEE	...A...A...L...G...V...P...F...I...G...I...N...N...	
F1.CY.08.CY222	M...T...N...L...	...L...A...I...S...A...I...L...V...T...F	...K...L...R...K...-...N...Y...E...R...-	...D...DAEE	...A...A...L...G...V...P...F...I...G...I...N...N...	
F1.ES.02.ES.X845.4	M...S...N...L...	...L...A...I...S...A...I...L...V...T...F	...K...L...R...K...-...N...Y...E...R...-	...D...DAEE	...A...A...L...G...V...P...F...I...G...I...N...N...	
F1.ES.11.VA0053.nfl1	M...L...Y...	...L...I...S...I...L...L...V...T...Y	...L...V...N...Y...E...I...R...	...D...DAEE	...A...D...L...G...V...P...F...I...G...I...N...N...	
F1.FR.04.LA221eRe	M...S...Y...L...	...L...A...I...S...A...I...L...V...T...F	...K...L...R...K...-...N...Y...E...I...R...	...D...DAEE	...A...A...L...G...V...P...F...I...G...I...N...N...	
F1.FR.03.LA26DuCl	M...S...Y...L...	...L...A...I...S...A...I...L...V...T...F	...K...L...R...K...-...N...Y...E...I...R...	...D...DAEE	...A...A...L...G...V...P...F...I...G...I...N...N...	
F1.RU.08.D88.845	M...T...E...I...	...L...I...G...-...I...L...V...T...F	...L...V...N...Y...E...I...R...	...D...DAEE	...A...A...L...G...V...P...F...I...G...I...N...N...	
F2.CM.02.02CM.0016BBY	M...S...Y...L...	...L...V...F...I...L...A...I...T...Y	...K...Q...-...K...R...N...Y...E...I...R...	...D...DAEE	...A...A...L...G...V...L...F...I...G...I...N...N...	
F2.CM.10.DEMF210CM007	M...S...L...S...	...L...V...F...I...L...A...I...T...Y	...K...L...-...K...R...N...Y...E...I...R...	...D...DAEE	...A...A...L...G...V...P...F...I...G...I...N...N...	
F2.CM.11.DEURF11CM026	M...S...L...V...	...L...A...G...-...I...L...I...T...Y...K	...L...V...K...R...N...W...F...E...S...	...D...DAEE	...A...A...L...G...V...P...F...I...G...I...N...N...	
G.CD.03.LA231Ed	M...L...L...	...A...-...G...I...F...L...A...I...T...F	...L...L...E...R...K...-...E...K...I...R...	...D...DTEE	...A...T...L...M...-...D...F...D...-...V...G...N...-	
G.CM.08.789.19	M...L...A...	...A...-...G...I...F...L...A...I...T...F	...L...L...E...R...K...-...E...K...I...R...	...D...DTEE	...A...T...L...M...-...D...F...D...-...V...G...N...-	
G.CM.10.DEMG10CM008	M...A...L...	...A...-...G...I...F...L...A...I...T...F	...L...L...E...R...K...-...E...K...I...R...	...D...DTEE	...A...T...L...M...-...D...F...D...-...V...G...N...-	
G.CM.10.DEURF10CM020	M...S...L...Q...	...A...S...G...-...F...A...T...I...T...Y	...-...R...K...R...K...-...K...N...I...R...	...D...DTEE	...S...T...L...D...V...D...F...D...-...V...G...N...-	
G.CM.08.GX.2084.08	M...L...E...	...A...-...G...I...F...A...I...T...Y...X	...R...K...R...K...I...L...I...R...	...D...DTEE	...S...T...L...D...V...D...F...D...-...V...G...N...-	
G.ES.14.ARP1201	M...L...V...	...F...S...G...-...F...A...I...T...Y...X	...R...K...R...K...I...L...I...R...	...D...DTEE	...S...T...L...D...V...D...F...D...-...V...G...N...-	
G.GH.03.03GH175G	M...S...L...E...	...V...S...G...I...S...A...I...T...Y...K	...L...V...N...Y...E...I...R...	...D...DTDE	...A...L...L...D...F...D...-...V...G...N...-	
G.GW.08.LAS71Me	M...L...E...	...A...S...G...I...F...L...A...I...T...F	...L...V...N...Y...E...I...R...	...D...DTDE	...A...L...L...D...F...D...-...V...G...N...-	
G.KE.09.DEMG09KE001	M...L...E...	...A...S...G...I...F...L...A...I...T...F	...L...V...N...Y...E...I...R...	...D...DEEE	...A...T...L...G...R...A...F...D...-...V...G...N...-	
G.NG.12.12NG060409	M...S...L...E...	...A...-...G...I...F...V...A...A...T...Y	...L...L...K...R...K...R...L...E...I...Q...	...D...DTEE	...A...T...L...D...V...D...F...E...-...V...G...N...-	
H.CD.04.LA19KoSa	M...S...L...Y...	...A...L...G...V...G...-...S...L...V...I...T...Y	...L...L...V...K...K...-...I...E...I...R...	...D...DAEE	...S...K...L...P...D...L...N...-...A...-	
H.CF.02.LA25LeM1	M...Y...I...L...	...T...I...G...-...I...F...V...I...T...Y...L	...V...K...R...L...E...I...R...	...D...DTEE	...S...T...L...R...Q...L...N...L...G...Y...A...-	
H.GB.00.00GBAC4001	M...Y...I...L...	...T...I...G...-...I...F...V...I...T...Y...L	...V...K...R...L...E...I...R...	...D...DTEE	...S...T...L...R...-...L...N...L...G...Y...A...-	
J.CD.03.LA26D1A0	M...L...L...	...I...-...I...-...S...L...L...G...T...V...Y	...L...L...N...K...-...I...R...	...D...DTDE	...S...K...L...P...D...L...N...-...A...-	
J.CD.07.J.97DC.KTB147	M...L...D...	...A...-...G...I...F...L...G...M...T...Y	...K...L...-...K...I...R...	...D...DTDE	...A...L...L...T...D...L...N...N...-	
J.SE.93.SE9280.7887	M...I...T...Q...	...A...-...F...I...F...L...G...M...T...Y	...K...L...-...K...I...R...	...D...DTDE	...A...L...L...T...D...L...N...N...-	
K.CD.97.97ZR.E0TB11	M...V...L...	...T...G...I...-...A...L...L...I...T...A...Y	...L...V...V...K...R...N...W...F...I...R...	...D...DTEE	...A...A...L...G...T...L...I...L...I...G...I...N...N...	
K.CM.96.96CM.MP535	M...V...S...L...	...A...I...S...-...I...L...I...T...Y...L	...V...K...R...N...W...F...I...R...	...D...DAEE	...A...D...I...G...L...L...I...L...I...G...I...N...N...	
01.AE.AF.07.569M	M...T...L...E...	...S...-...G...I...L...S...T...-...A...-...A	...K...L...-...K...R...K...V...K...I...R...	...D...DTEE	...W...A...K...L...-...D...F...D...-...V...G...N...-	
01.AE.CM.11.1156.26	M...N...A...L...	...W...-...G...V...L...V...A...-...K	...K...R...K...V...K...I...R...	...D...DTDE	...A...T...L...D...F...D...H...-...V...G...N...-	
01.AE.CM.12.DE00112CN011	M...T...L...E...	...S...-...G...I...L...L...T...V...A...L...I	...I...-...K...R...I...E...I...R...	...D...DTEE	...A...K...L...N...F...D...-...V...G...N...-	
01.AE.HK.04.HK001	M...T...L...Q...	...S...-...G...I...L...L...T...G...L...V	...-...K...K...I...R...E...I...R...	...D...DTEE	...A...K...L...D...F...D...-...V...G...N...-	
01.AE.IR.10.10IR.THR48F	M...T...L...E...	...S...-...A...G...-...L...L...T...A...-...R	...F...N...-...K...I...S...X...-...E...	...D...DTEE	...A...K...L...D...F...D...-...V...G...N...-	
01.AE.IP.11.DE00111JP003	M...T...L...Q...	...S...-...A...G...-...L...L...T...A...-...R	...F...N...-...K...I...S...X...-...E...	...D...DTEE	...A...K...L...D...F...D...-...V...G...N...-	
01.AE.SE.11.SE601018	M...N...S...L...	...E...S...-...A...G...I...L...L...T...A...Q	...I...-...Q...K...K...I...R...K...I...R...	...D...DTDE	...D...K...L...D...F...D...-...V...G...N...Y...	
01.AE.TH.10.DE00110TH001	M...T...H...L...	...E...S...-...G...I...L...L...T...A...-...F	...K...-...K...I...R...			

	transmembrane domain		phos		phos		Vpu end
	Vpu start		α-helix		α-helix		
B. FR. 83. HXB2	M-L	E	A-G	F-A	T-Y	A	...
02 AG. KR. 12. 12MHI11 10746	M-L	E	S-G	I-F	A-V	T	...
02 AG. KR. 12. 12MHR9	M-L	E	A-G	F-A	T-Y	A	...
02 AG. LR. x. P0C44951	M-L	E	A-G	F-A	T-Y	A	...
02 AG. NG. 12. 12NG0660418	MNSL	E	T-G	I-F	A-V	T	...
02 AG. NG. x. I1BNC	M-L	T	A-G	F-A	T-Y	A	...
02 AG. SN. x. I1E602024	M-SL	E	A-G	F-A	T-Y	A	...
02 AG. SN. 13. 9580	M-SL	T	A-G	F-A	T-Y	A	...
03 AB. RU. 97. KAL153 2	M-SL	A	A-G	F-A	T-Y	A	...
04 cpd. CY. 94. 94CY032 3	MLFW	E	W-G	L-V	T-F	K-L	...
05 DF. BE. x. V1110	MSDL	L	TI-V	I-L	T-Y	K-L	...
06 cpd. AU. 96. BFP90	M-AL	E	A-G	F-FLA	I-T	Y-Q	...
07 BC. CN. 98. 98CN009	M-TL	E	A-G	F-A	T-Y	A	...
08 BC. CN. 97. 97CNGX 6F	MLDL	L	EL-VG	I-L	T-Y	RL	...
09 cpd. GH. 96. 96GH2911	M-SL	Q	AS-G	GII-F	A-IA	T-F	...
10 CD. TZ. 96. 96TZ BF061	MNSL	L	LARVYKLRV	G-I	L-T	Y-Q	...
11 cpd. CN. 95. 95CN 1816	MISL	Q	AS-I	F-V	T-GL	L-L	...
12 BF. AR. 99. ARMA159	M-SL	V	TL	AV	T-L	Y-L	...
13 cpd. CM. 96. 96CM 1849	MNAL	L	IS	I-F	V-T	AY	...
14 BG. ES. 05. X1870	M-SL	E	A-G	I-G	A-X	T-F	...
15 01B. TH. 99. 99TH MU2079	MS-L	E	S-G	I-L	T-L	A-I	...
16 AZD. KR. 97. 97KR004	MNSL	Q	LS-G	I-L	V-L	T-Y	...
17 BF. AR. 99. ARMA038	M-AL	I	AS	I-T	L-V	T-Y	...
18 cpd. CU. 99. CU76	MXXF	E	G-I	I-F	VC	T-Y	...
19 cpd. CU. 99. CU7	M-AL	Q	A-G	I-F	A-T	Y	...
20 BG. CU. 99. CU103	M-SL	E	VA	G-I	G-A	I-A	...
21 AZD. KE. 99. KER2003	M-AL	Q	I	A-G	I-L	T-L	...
22 01A1. CM. 01. 011CM 0001BBY	M-TL	E	CT	G-I	L-L	T-Y	...
23 BG. CU. 03. CB118	MNSL	E	A-V	G-I	G-A	I-A	...
24 BG. ES. 08. X2456 2	M-SL	E	A-G	I-C	A-I	T-W	...
25 cpd. CM. 02. 1918LE	M-SL	E	F	G-I	F-V	VI	...
26 AU. CD. 02. 02CD MBT0047	MT-L	Q	Y	G-I	F-L	V	...
27 cpd. FR. 04. 04FR K25	M-SL	Q	TIS	A-I	F-L	V	...
28 BF. BR. 99. BREP12609	M-AL	I	I	A-VA	T-F	L	...
29 BF. BR. 01. BREPM16704	M-SL	Q	I	G-VA	T-F	L	...
31 BC. BR. 04. 04BR142	MFTL	L	ERIDYR	G-G	L-L	I-T	...
32 06A1. EE. 01. EE0369	M-AL	E	S	G-I	II	SLA	...
33 01B. ID. 07. JKT185 C	MS-L	E	S	AG	II	L-L	...
34 01B. TH. 99. QUR1969P	S	S	G-I	L-L	T-L	G	...
35 AD. AF. 07. 169H	MTSL	Y	W	AG	L-L	T-G	...
36 cpd. CM. 00. 00CMNYU830	M-SL	Q	A	AG	F-A	GG	...
37 cpd. CM. 00. 00CMNYU926	M-L	E	YS	G-I	F-A	T-L	...
38 BFI. UY. 03. UY03 3389	MNSL	L	VLG	I-L	T-L	AYL	...
39 BF. BR. 04. 04BR3179	MSDL	Q	AIG	T-I	F-A	I	...
40 BF. BR. 05. 05BRR1055	M-SL	Q	A	G-VA	T-L	L-L	...
42 BF. LU. 03. LuBF 01 03	M-SL	V	L	G-A	V-L	T-L	...
43 02G. SA. 03. J11223	M-XL	E	A	G-I	FLA	T-F	...
44 BF. CL. 00. CH80	MTDL	L	AIS	A-I	A-V	I-Y	...
45 cpd. FR. 04. 04FR AUK	MNYL	L	G	A-T	ALL	I-T	...
46 BF. BR. 07. 07BR FPS625	MSDL	L	AISLA	I-A	ALL	I-T	...
47 BF. ES. 08. P1942	M-SL	E	L	G-A	L-L	T-L	...
48 01B. MY. 07. 07MYKT021	MT-L	Q	VS	G-L	L-L	T-L	...
49 cpd. GM. 03. N26677	M-SL	Q	A	A-I	F	FLV	...
50 A1D. GB. 10. 12792	M-L	V	LS	A-IVS	I-T	F	...
51 01B. SG. 11. 11SG HM021	MSSL	D	L	S	G-I	L-L	...
52 01B. MY. 03. 03MYK1018 1	M-L	E	S	AG	L-L	T-A	...
53 01B. MY. 11. 11FIR164	MT-L	Q	S	G-L	L-L	T-VL	...
54 01B. MY. 09. 09MYSB023	MT-L	Q	S	AG	I-L	L-T	...
55 01B. CN. 10. HNC5102056	MT-L	E	S	AG	I-L	L-T	...
56 cpd. FR. 10. URFS patient A	M-L	E	A	G-I	F-A	I-T	...
57 BC. CN. 09. 09YNLX1959	MLN	L	IN	YRLGVG	L-L	T-Y	...
58 01B. MY. 09. 09MYP37	MS-L	E	S	G-I	L-L	T-A	...
59 01B. CN. 09. 09LNA423	MNSL	ET	GV	I-F	IVG	T-L	...
60 BC. IT. 11. BAV499	MLG5	L	IDYRLGVG	I-RL	I-Y	L-V	...
61 BC. CN. 10. J1100010	M-L	V	LESAL	VG	L-V	T-L	...
62 BC. CN. 10. YNFL13	M-SL	T	LS	G-I	L-L	T-F	...
63 02A1. RU. 10. 10RU6637	M-TL	E	A	G-F	A-T	Y	...
64 BC. CN. 09. YNFL31	MLDL	L	NYTITV	G-FI	L-L	T-Y	...
65 cpd. CN. 10. YNFL01	M-L	V	S	G-I	L-L	T-L	...
67 01B. CN. 11. ANHUI HF115	MT-L	E	S	G-I	L-L	X-T	...
68 01B. CN. 11. ANHUI WH73	MT-L	E	S	G-I	L-L	X-T	...
69 01B. JP. 05. 05JPMYC113SP420	M-TL	E	W	AG	II	L-L	...
70 BFI. BR. 10. 10BR PE004	M-SL	L	YS	VA	T-L	L	...
71 BFI. BR. 10. 10BR PE008	MP-L	Y	L	G-L	I-L	T-L	...
72 BFI. BR. 10. 10BR MG002	MT-L	Y	S	G-I	G-L	I-T	...
73 BG. DE. 01. 9196 01	MS-L	Q	S	G-I	L-A	T-L	...
74 01B. MY. 10. 10MYP268	MNSL	Q	S	AG	I-L	L-L	...
78 cpd. CN. 13. YNCT19	M-TL	E	I	FS	VA	T-L	...
85 BC. CN. 14. 14CN SCYB2	M-L	Y	ISLGL	VA	T-L	L	...
86 BC. CN. 13. 15YNHS18	M-SL	Y	ISLGL	VA	T-L	L	...
87 cpd. CN. 12. DH32	M-AL	L	V	DYRLGVG	I-V	T-Y	...
88 BC. CN. 05. 05YNRL259g	MLD	L	V	DYRLGVG	I-V	T-Y	...
0. CM. 96. LA51YBF35	MHW	G	L	LII	F5	CLL	...
0. CM. 96. LA52YBF39	MPHK	G	L	LII	II	ALLL	...
0. CM. 99. CM04122	M-HK	D	L	LII	LII	SALL	...
0. CM. x. pCM02 3	M-HR	D	L	LII	LII	SALL	...
0. ES. 01. Rea025 HIV Group 0	MHYR	G	L	LII	LII	SALL	...
0. FR. 06. LA55RBF206	MHOR	D	L	LII	LII	SALL	...
0. GA. 11. 11IGab6352	M-HK	D	L	LII	LII	SALL	...
0. SN. 99. 99SE MP1299	MHRH	D	L	LII	LII	SALL	...
0. SN. 99. 99SE MP1300	MHRH	D	L	LII	LII	SALL	...
0. US. 10. LTNP	M-HK	D	L	LII	LII	SALL	...
N. CM. 06. U14296	MLQ	Q	S	FT	G-L	V-I	...
N. FR. 11. N1 FR 2011	MLG	L	L	GF	VG	F-V	...
P. CM. 06. U14788	MH-R	D	E	AV	LII	AG	...
P. FR. 09. RBF168	MH-R	D	E	AV	LII	AG	...
CPZ. TZ. 06. TAN5	VGSL	L	L	TNV	GIF	CILL	...
CPZ. US. 85. US Marilyn	MLNW	F	L	E	IGL	GIEG	...
GOR. CN. 12. SIVgor_B0ID2	MHYR	G	L	LII	LII	SALL	...
GOR. CN. 13. SIVgor_BPID15	MHYR	G	L	LII	LII	SALL	...



Table with columns: Env start, signal peptide end\_gp120 start, glycosylation NVT, glycosylation NDT, CD4 binding, and protein ID. Rows list various HIV-1 protein sequences and their glycosylation sites.

	glycosylation NCS			glycosylation NTS			CD4 binding			glycosylation NVS		
	glycosylation NCS			glycosylation NDT			glycosylation NTS			glycosylation NGT		
	glycosylation NCS			glycosylation NDT			glycosylation NTS			glycosylation NKT		
	glycosylation NCS			glycosylation NDT			glycosylation NTS			glycosylation NKT		
B.FR.83.HXB2	..	..	..	..	..	..	..	..	..	..	..	..
A1.CM.08.886.24	..	..	..	..	..	..	..	..	..	..	..	..
A1.CY.08.CY236	..	..	..	..	..	..	..	..	..	..	..	..
A1.KE.11.DEMA111KE002	..	..	..	..	..	..	..	..	..	..	..	..
A1.NG.10.10NG040248	..	..	..	..	..	..	..	..	..	..	..	..
A1.PK.14.DEMA114PK001	..	..	..	..	..	..	..	..	..	..	..	..
A1.RW.11.DEMA111RW002	..	..	..	..	..	..	..	..	..	..	..	..
A1.UG.11.DEMA110UG009	..	..	..	..	..	..	..	..	..	..	..	..
A1.ZA.04.503.15344.T10.A1	..	..	..	..	..	..	..	..	..	..	..	..
A2.CM.01.01CM.1445MV	..	..	..	..	..	..	..	..	..	..	..	..
A3.SN.01.DD1579	..	..	..	..	..	..	..	..	..	..	..	..
A4.CD.97.97CD.KCC2	..	..	..	..	..	..	..	..	..	..	..	..
A6.BY.13.PV85	..	..	..	..	..	..	..	..	..	..	..	..
A6.CY.09.CY255	..	..	..	..	..	..	..	..	..	..	..	..
A6.RU.11.1RU06950	..	..	..	..	..	..	..	..	..	..	..	..
A6.UA.12.DEMA112UA014	..	..	..	..	..	..	..	..	..	..	..	..
B.BR.10.10BR.RJ032	..	..	..	..	..	..	..	..	..	..	..	..
B.CA.07.502.1191.03	..	..	..	..	..	..	..	..	..	..	..	..
B.CH.08.M2.0803101.NFLG8	..	..	..	..	..	..	..	..	..	..	..	..
B.CN.12.DEMB12CN006	..	..	..	..	..	..	..	..	..	..	..	..
B.CU.14.14CU085	..	..	..	..	..	..	..	..	..	..	..	..
B.DE.13.366396	..	..	..	..	..	..	..	..	..	..	..	..
B.ES.14.ARP1495	..	..	..	..	..	..	..	..	..	..	..	..
B.FR.11.DEMB11FR001	..	..	..	..	..	..	..	..	..	..	..	..
B.HT.05.05HT.129389	..	..	..	..	..	..	..	..	..	..	..	..
B.JP.12.DEMB12JP001	..	..	..	..	..	..	..	..	..	..	..	..
B.KR.07.HP.18.07JHS10.3909	..	..	..	..	..	..	..	..	..	..	..	..
B.RU.11.11RU021	..	..	..	..	..	..	..	..	..	..	..	..
B.SE.12.SEG00057	..	..	..	..	..	..	..	..	..	..	..	..
B.TH.10.DEMB10TH002	..	..	..	..	..	..	..	..	..	..	..	..
B.US.16.2609	..	..	..	..	..	..	..	..	..	..	..	..
C.BR.11.DEMC11BR035	..	..	..	..	..	..	..	..	..	..	..	..
C.CN.10.YNFI19	..	..	..	..	..	..	..	..	..	..	..	..
C.DE.10.622166	..	..	..	..	..	..	..	..	..	..	..	..
C.ES.14.ARP1498	..	..	..	..	..	..	..	..	..	..	..	..
C.ET.08.ET104	..	..	..	..	..	..	..	..	..	..	..	..
C.IN.15.NIRT008	..	..	..	..	..	..	..	..	..	..	..	..
C.MW.09.703010256.CH256.w96	..	..	..	..	..	..	..	..	..	..	..	..
C.NG.10.10NG082523	..	..	..	..	..	..	..	..	..	..	..	..
C.NP.11.11NP01	..	..	..	..	..	..	..	..	..	..	..	..
C.PK.14.DEMC14PK009	..	..	..	..	..	..	..	..	..	..	..	..
C.SE.13.SEG000311	..	..	..	..	..	..	..	..	..	..	..	..
C.TZ.08.707010457.CH457.w8	..	..	..	..	..	..	..	..	..	..	..	..
C.US.11.17T84.4G8	..	..	..	..	..	..	..	..	..	..	..	..
C.ZA.13.DEMC13ZA152	..	..	..	..	..	..	..	..	..	..	..	..
C.ZM.11.DEMC11ZM006	..	..	..	..	..	..	..	..	..	..	..	..
D.BR.10.10BR.RJ108	..	..	..	..	..	..	..	..	..	..	..	..
D.CD.03.LA17Mu0	..	..	..	..	..	..	..	..	..	..	..	..
D.CM.10.DEMD10CM009	..	..	..	..	..	..	..	..	..	..	..	..
D.CY.06.CY163	..	..	..	..	..	..	..	..	..	..	..	..
D.KE.11.DEMD11KE003	..	..	..	..	..	..	..	..	..	..	..	..
D.KR.04.04KR08	..	..	..	..	..	..	..	..	..	..	..	..
D.KZ.01.288	..	..	..	..	..	..	..	..	..	..	..	..
D.UG.10.DEMD10UG004	..	..	..	..	..	..	..	..	..	..	..	..
D.UG.11.DEMD11UG003	..	..	..	..	..	..	..	..	..	..	..	..
D.YE.02.02YE516	..	..	..	..	..	..	..	..	..	..	..	..
F1.A0.06.A0.06.ANG32	..	..	..	..	..	..	..	..	..	..	..	..
F1.AR.02.ARE933	..	..	..	..	..	..	..	..	..	..	..	..
F1.BR.10.10BR.RJ015	..	..	..	..	..	..	..	..	..	..	..	..
F1.FR.11.DEMF11BR037	..	..	..	..	..	..	..	..	..	..	..	..
F1.CY.08.CY222	..	..	..	..	..	..	..	..	..	..	..	..
F1.E5.02.E5.X845.4	..	..	..	..	..	..	..	..	..	..	..	..
F1.E5.11.VA0053.nf1	..	..	..	..	..	..	..	..	..	..	..	..
F1.FR.04.LA221.re	..	..	..	..	..	..	..	..	..	..	..	..
F1.R0.03.LA20DUC1	..	..	..	..	..	..	..	..	..	..	..	..
F1.RU.08.D88.845	..	..	..	..	..	..	..	..	..	..	..	..
F2.CM.02.02CM.0016BBY	..	..	..	..	..	..	..	..	..	..	..	..
F2.CM.10.DEMF210CM007	..	..	..	..	..	..	..	..	..	..	..	..
F2.CM.11.DEURF11CM026	..	..	..	..	..	..	..	..	..	..	..	..
G.CD.03.LA23L1ed	..	..	..	..	..	..	..	..	..	..	..	..
G.CM.08.709.10	..	..	..	..	..	..	..	..	..	..	..	..
G.CM.10.DEMG10CM008	..	..	..	..	..	..	..	..	..	..	..	..
G.CM.10.DEURF10CM020	..	..	..	..	..	..	..	..	..	..	..	..
G.CN.08.GX.2084.08	..	..	..	..	..	..	..	..	..	..	..	..
G.E5.14.ARP1201	..	..	..	..	..	..	..	..	..	..	..	..
G.GH.03.03GH175G	..	..	..	..	..	..	..	..	..	..	..	..
G.GK.08.LAS71.nf6	..	..	..	..	..	..	..	..	..	..	..	..
G.KE.09.DEMG09KE001	..	..	..	..	..	..	..	..	..	..	..	..
G.NG.12.12NG060409	..	..	..	..	..	..	..	..	..	..	..	..
H.CD.04.LA19Ko5a	..	..	..	..	..	..	..	..	..	..	..	..
H.CF.02.LA25LeM1	..	..	..	..	..	..	..	..	..	..	..	..
H.GB.00.00GBCA4001	..	..	..	..	..	..	..	..	..	..	..	..
J.CD.03.LA26D1An	..	..	..	..	..	..	..	..	..	..	..	..
J.CD.07.J.97Dc.KTB147	..	..	..	..	..	..	..	..	..	..	..	..
J.SE.93.SEB280.7887	..	..	..	..	..	..	..	..	..	..	..	..
K.CD.97.97ZR.E0T811	..	..	..	..	..	..	..	..	..	..	..	..
K.CM.96.96CM.MP535	..	..	..	..	..	..	..	..	..	..	..	..
01.AE.AF.07.569M	..	..	..	..	..	..	..	..	..	..	..	..
01.AE.CM.11.1156.26	..	..	..	..	..	..	..	..	..	..	..	..
01.AE.CN.12.DE00112CN011	..	..	..	..	..	..	..	..	..	..	..	..
01.AE.HK.04.HK001	..	..	..	..	..	..	..	..	..	..	..	..
01.AE.IR.10.10IR.THR48F	..	..	..	..	..	..	..	..	..	..	..	..
01.AE.JP.11.DE00111JP003	..	..	..	..	..	..	..	..	..	..	..	..
01.AE.SE.11.SEG01018	..	..	..	..	..	..	..	..	..	..	..	..
01.AE.TH.10.DE00110TH001	..	..	..	..	..	..	..	..	..	..	..	..
01.AE.UH.90.CM240	..	..	..	..	..	..	..	..	..	..	..	..
01.AE.US.05.306163.FL	..	..	..	..	..	..	..	..	..	..	..	..
02.AG.CM.10.DE00210CM013	..	..	..	..	..	..	..	..	..	..	..	..
02.AG.DE.09.081114	..	..	..	..	..	..	..	..	..	..	..	..
02.AG.GW.05.CC.0048	..	..	..	..	..	..	..	..	..	..	..	..

	glycosylation NVS										
	glycosylation NNT		glycosylation NTS				glycosylation NGT				
	V1	V2	CD4 binding		glycosylation NTS		glycosylation NGT		glycosylation NKT		
B. FR. 83. HXB2	.....NSSS.....	.GR.MI..MEKGEIKNCSFNISTSRIGVKV.KEYAFFYKLDIIPDNDT.....			.TSYKLTSCNVSITQACPVKVSFEPIPIHYCAPAGFAILKNCKNFTNGTGTCTNVSTVQC <th>THGIRPVVS</th> <td colspan="4"></td>		THGIRPVVS				
02 AG. KR. 12. 12MHI11 10746	.....NI.TD..EMR.....	.VT.EL.DTKK.NVF.L.R.VKQ.NENNS..AQ.....	YDSTK..SQ.R.IN..S.A.....	I.....	R.....	.DDEE.T..L.K.....	G.L.....				
02 AG. KR. 12. 12MHR9	.....SI.SS..DMRE.....	.T.MT.EV.D.K..VS.L.RY.VQ.NENKN.....	.....SS..SQ.R.IN..A.....	T.....	.....	.K.....	K.....				
02 AG. LR. x. POC44951	.....LN.DTQE..R.....	.VT.EL.D.K..V.L.R.VQ.N.SKGK..S.....	KND..SQ.R.VN..A.....	T.....	.....	.SDEK.K..Q.K.....	K.....				
02 AG. NG. 12. 12N6066418	.....NF.TD..ELR.....	.MT.EL.DRK..VE.L.RQ.VS.FENKN..P.....	SH.R.IN..A.....	S.....	.....	.RK.Q.S..S.N.....	K.....				
02 AG. NG. x. IBN5	.....NL.TS..DMN.....	.T.EV.D.KK..VH.L.R.VQ.NENKN.....	SO.R.IN..A.....	T.....	.....	.K.D.G.....	K.....				
02 AG. SN. 13. 9580	.....I.C.....	.K.R.T.H.....	.ATAUL.D.Q..E.SL..R.V.Q.O.NING.....	.....	.....	.SIFR..T.....	T.....	Y.....	K.....	S.....	
02 AB. RU. 97. KAL153 2	.....MTR.....	.TV.FP..DM.....	.MT.VL.D.KE..VTS#..RQ.#VQ..A.T..CDNT..TCDNRTQV#..AR..IN..A.....	I.....	.....	.D.N.....	K.....				
04 CPX. CY. 94. 94CY032 3	.....TNT.SS..IKMM..M.....	.T.DL.D.K..L.....	VVO.....	R.I..V.....	.....	.D.K.....	K.....				
95 DF. BE. x. VT110	.....TTN.....	.GT.VT.EG..D.T.E.D.KK..L.RI..V..NARVPING.SN..RNNST..EE..M..IN..A.....	T.V.....	I.....	.....	.E.N.T.L.....	S.R.....				
06 CPX. AU. 96. BFP90	.....TTN.....	.TI.VL..AVQ.....	.MT.VND..VH.L.R.V..S.DS.....	SN.....	SD.R.IN..A.....	.....	WD.....	Y.....	K.....	K.....	
07 BC. CN. 98. 98CN009	.....NS.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
08 BC. CN. 97. 97CN6X 6F	.....TCN.....	.ET.CR..ESMK..K.....	.AT.VV.D.K..TV..L.R.V..FTKNS..S.....	GNSS..EH..R..IN..A.....	A.....	T.D.....	T.Y.....	DRR.....	H.....	K.....	
09 CPX. GH. 96. 96GH2911	.....TYN.....	.ET.YN..ESVK.....	.AT.L.DRKK.TV..L.R.V..LNDENS..G.....	ENSS..EY..R..IN..A.....	T.D.....	T.Y.....	D.I.....	O.H.....	K.....	K.....	
11 CD. TZ. 96. 96TZ03 3	.....TTLGNS.....	.CT.....	.NS.TV..EQQA..M.....	.T.E.D.QK.Q..L.....	VV..MNDWN.....	R..IN..A.....	T.....	.....	I.....	DRK.....	
16 AZD. KR. 97. 97KR001	.....WN.....	.....	.NS.TV..EQQA..M.....	.T.E.D.QK.Q..L.....	VV..MNDWN.....	R..IN..A.....	T.....	.....	I.....	DRK.....	
12 BF. AR. 99. ARMA159	.....VN.....	.....	.SS.TV..QGRF.....	.Y.M.T.GDGRR..V.SL.RV..E.EGNSN..S.....	GNSSS..SE..R.....	I.....	K.....	T.....	DEE.....	R.S.....	
13 CPX. CM. 96. 96CM 1849	.....KT.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
14 BG. ES. 05. X1870	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
15 01B. TH. 99. 99TH MU2079	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
16 AZD. KR. 97. 97KR001	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
17 BF. AR. 99. ARMA038	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
18 CPX. CU. 99. CU76	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
19 CPX. CU. 99. CU7	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
20 BG. CU. 99. CU103	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
21 AZD. KR. 97. 97KR001	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
22 01A1. CM. 01. 011CM 0001BBY	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
23 BG. CU. 03. CB118	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
24 BG. ES. 08. X2456 2	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
25 CPX. CM. 02. 1918E	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
26 AU. CD. 02. 02CD MBT047	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
45 CPX. FR. 04. 04FR AUK	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
28 BF. BR. 99. BREPM12609	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
29 BF. BR. 01. BREPM16704	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
31 BC. BR. 04. 04BR142	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
32 06A1. EE. 01. EE0369	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
33 01B. ID. 07. JKT189 C	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
34 01B. TH. 99. 99TH1969P	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
35 AD. AF. 07. 169H	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
36 CPX. CM. 00. 00CMNYU830	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
37 CPX. CM. 00. 00CMNYU926	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
38 BFI. UY. 03. UY03 3389	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
39 BF. BR. 04. 04BR13179	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
40 BF. BR. 05. 05BRR1055	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
42 BF. LU. 03. LU0F 01 03	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
43 02G. SA. 03. J11223	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
44 BF. CL. 08. CH80	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
45 CPX. FR. 04. 04FR AUK	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
46 BF. BR. 07. 07BR FPS625	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
47 BF. ES. 08. P1942	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
48 01B. MY. 07. 07MYKT021	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
49 CPX. GM. 03. N26677	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
50 A10. GB. 10. 12792	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
51 01B. SG. 10. 125G HM021	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
52 01B. MY. 03. 03MYK1018 1	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
53 01B. MY. 11. 11F1R164	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
54 01B. MY. 09. 09MYSB023	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
55 01B. CN. 10. 10NC182056	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
56 CPX. FR. 01. 01FR patient A	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
57 BC. CN. 09. 09YNLU1959	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
58 01B. MY. 09. 09MYPR37	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
59 01B. CN. 09. 09LNA423	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
60 BC. IT. 11. BAV499	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
61 BC. CN. 10. J1100010	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
62 BC. CN. 10. YNF13	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
63 02A1. RU. 10. 10RU6637	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
64 BC. CN. 09. YNF131	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
65 CPX. CN. 10. YNF101	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
67 01B. CN. 11. ANHUI HF115	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
68 01B. CN. 11. ANHUI WH73	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
69 01B. JP. 05. 05JPMYC113SP420	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
70 BFI. BR. 10. 10BR PE004	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
71 BFI. BR. 10. 10BR PE008	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
72 BFI. BR. 10. 10BR MG002	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
73 BG. DE. 01. 01D95	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
74 01B. MY. 10. 10MYPR268	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
78 CPX. CN. 13. YNCT19	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
85 BC. CN. 14. 14CN SCYB2	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
86 BC. CN. 13. 13YNSH18	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
87 CPX. CN. 12. DH32	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
88 BC. CN. 05. 05YNRL259g	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
0. CM. 96. LA51YBF35	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
0. CM. 96. LA52YBF39	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
0. CM. 99. 99CMU4122	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
0. CM. x. pCM02 3	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
0. ES. 01. Rea055 HIV Group0	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
0. FR. 06. LA55RBF206	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
0. GA. 11. 11GAb6352	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
0. SN. 99. 99SE MP1290	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
0. SN. 99. 99SE MP1300	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
0. US. 10. LTNP	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
N. CM. 06. U14206	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
N. FR. 11. FR. 2011	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
P. CM. 06. U14788	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
P. FR. 09. RBF168	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
CPZ. TZ. 06. TAN5	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
CPZ. US. 85. US Marilyn	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
GOR. CM. 12. SIVgor B01D2	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	
GOR. CM. 13. SIVgor_BP1D5	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	

	glycosylation NGS	glycosylation NFT	glycosylation NCT	V3 tip	glycosylation NNT	glycosylation NKT	CD4 binding
B.FR.83.HXB2	.....	.....	.....	.....	.....	.....	.....
A1.CM.08.886.24	.....	.....	.....	.....	.....	.....	.....
A1.CY.08.CY236	.....	.....	.....	.....	.....	.....	.....
A1.KE.11.DEM111KE002	.....	.....	.....	.....	.....	.....	.....
A1.NG.10.10NG040248	.....	.....	.....	.....	.....	.....	.....
A1.PK.14.DEM1114PK001	.....	.....	.....	.....	.....	.....	.....
A1.RW.11.DEM111RW002	.....	.....	.....	.....	.....	.....	.....
A1.UG.11.DEM111UG009	.....	.....	.....	.....	.....	.....	.....
A1.ZA.04.503.15344.T10.A1	.....	.....	.....	.....	.....	.....	.....
A2.CM.01.01CM.1445MV	.....	.....	.....	.....	.....	.....	.....
A3.SN.01.DD1579	.....	.....	.....	.....	.....	.....	.....
A4.CD.97.97CD.KCC2	.....	.....	.....	.....	.....	.....	.....
A6.BY.13.PV85	.....	.....	.....	.....	.....	.....	.....
A6.CY.09.CY255	.....	.....	.....	.....	.....	.....	.....
A6.RU.11.1RU06950	.....	.....	.....	.....	.....	.....	.....
A6.UA.12.DEM112UA014	.....	.....	.....	.....	.....	.....	.....
B.BR.10.10BR.R1032	.....	.....	.....	.....	.....	.....	.....
B.CA.07.502.1191.03	.....	.....	.....	.....	.....	.....	.....
B.CH.08.M2.0803101.NFLG8	.....	.....	.....	.....	.....	.....	.....
B.CN.12.DEM12CN006	.....	.....	.....	.....	.....	.....	.....
B.CU.14.14CU005	.....	.....	.....	.....	.....	.....	.....
B.DE.13.366396	.....	.....	.....	.....	.....	.....	.....
B.EC.14.ARP1495	.....	.....	.....	.....	.....	.....	.....
B.FR.11.DEM11FR001	.....	.....	.....	.....	.....	.....	.....
B.HT.05.05HT.129389	.....	.....	.....	.....	.....	.....	.....
B.JP.12.DEM12JP001	.....	.....	.....	.....	.....	.....	.....
B.KR.07.HP.18.07JHS10.3909	.....	.....	.....	.....	.....	.....	.....
B.RU.11.11RU021	.....	.....	.....	.....	.....	.....	.....
B.SE.12.5E600057	.....	.....	.....	.....	.....	.....	.....
B.TH.10.DEM110TH002	.....	.....	.....	.....	.....	.....	.....
B.US.16.2609	.....	.....	.....	.....	.....	.....	.....
C.BR.11.DEM11BR035	.....	.....	.....	.....	.....	.....	.....
C.CN.10.YNFI19	.....	.....	.....	.....	.....	.....	.....
C.DE.10.622166	.....	.....	.....	.....	.....	.....	.....
C.IS.14.ARP1498	.....	.....	.....	.....	.....	.....	.....
C.ET.08.ET104	.....	.....	.....	.....	.....	.....	.....
C.IN.15.NIRT008	.....	.....	.....	.....	.....	.....	.....
C.MW.09.703010256.CH256.W96	.....	.....	.....	.....	.....	.....	.....
C.NG.10.10NG082523	.....	.....	.....	.....	.....	.....	.....
C.NP.11.11NP016	.....	.....	.....	.....	.....	.....	.....
C.PK.14.DEM14PK009	.....	.....	.....	.....	.....	.....	.....
C.SE.13.5E600311	.....	.....	.....	.....	.....	.....	.....
C.TZ.08.707010457.CH457.W8	.....	.....	.....	.....	.....	.....	.....
C.US.11.17784.4G8	.....	.....	.....	.....	.....	.....	.....
C.ZA.13.DEM13ZA152	.....	.....	.....	.....	.....	.....	.....
C.ZM.14.DEM14ZM006	.....	.....	.....	.....	.....	.....	.....
D.BR.10.10BR.R1108	.....	.....	.....	.....	.....	.....	.....
D.CD.03.LA17Mu0o	.....	.....	.....	.....	.....	.....	.....
D.CM.10.DEM10CM009	.....	.....	.....	.....	.....	.....	.....
D.CY.06.CY163	.....	.....	.....	.....	.....	.....	.....
D.KE.11.DEM11KE003	.....	.....	.....	.....	.....	.....	.....
D.KR.04.04KR04	.....	.....	.....	.....	.....	.....	.....
D.ZI.01.Z288	.....	.....	.....	.....	.....	.....	.....
D.UG.10.DEM10UG004	.....	.....	.....	.....	.....	.....	.....
D.UG.11.DEM11UG003	.....	.....	.....	.....	.....	.....	.....
D.YE.02.02YE516	.....	.....	.....	.....	.....	.....	.....
F1.A0.06.A0.06.ANG32	.....	.....	.....	.....	.....	.....	.....
F1.AR.02.ARE933	.....	.....	.....	.....	.....	.....	.....
F1.BR.10.10BR.RJ015	.....	.....	.....	.....	.....	.....	.....
F1.FR.11.DEMF11BR037	.....	.....	.....	.....	.....	.....	.....
F1.CY.08.CY222	.....	.....	.....	.....	.....	.....	.....
F1.ES.02.ES.X845.4	.....	.....	.....	.....	.....	.....	.....
F1.ES.11.VA0053.nfl	.....	.....	.....	.....	.....	.....	.....
F1.FR.04.LA21rre	.....	.....	.....	.....	.....	.....	.....
F1.R0.03.LA20DUC1	.....	.....	.....	.....	.....	.....	.....
F1.RU.08.D88.845	.....	.....	.....	.....	.....	.....	.....
F2.CM.02.02CM.0016BBY	.....	.....	.....	.....	.....	.....	.....
F2.CM.10.DEMF210CM007	.....	.....	.....	.....	.....	.....	.....
F2.CM.11.DEURF21CM026	.....	.....	.....	.....	.....	.....	.....
G.CD.03.LA23L1Ed	.....	.....	.....	.....	.....	.....	.....
G.CM.08.709.10	.....	.....	.....	.....	.....	.....	.....
G.CM.10.DEMG10CM008	.....	.....	.....	.....	.....	.....	.....
G.CM.10.DEURF10CM020	.....	.....	.....	.....	.....	.....	.....
G.CN.08.GX.2084.08	.....	.....	.....	.....	.....	.....	.....
G.ES.14.ARP1201	.....	.....	.....	.....	.....	.....	.....
G.GH.03.03GH1756	.....	.....	.....	.....	.....	.....	.....
G.GH.08.LAS.71Mne	.....	.....	.....	.....	.....	.....	.....
G.KE.09.DEMG09KE001	.....	.....	.....	.....	.....	.....	.....
G.NG.12.12NG0606009	.....	.....	.....	.....	.....	.....	.....
H.CD.04.LA19Ko5a	.....	.....	.....	.....	.....	.....	.....
H.CF.02.LA25LeM1	.....	.....	.....	.....	.....	.....	.....
H.GB.00.00GBAC4001	.....	.....	.....	.....	.....	.....	.....
J.CD.03.LA26D1A0	.....	.....	.....	.....	.....	.....	.....
J.CD.07.1.970C.KTB147	.....	.....	.....	.....	.....	.....	.....
J.SE.93.5E9280.7887	.....	.....	.....	.....	.....	.....	.....
K.CD.97.97ZR.E0T811	.....	.....	.....	.....	.....	.....	.....
K.CM.96.96CM.MP535	.....	.....	.....	.....	.....	.....	.....
01.AE.AF.07.569M	.....	.....	.....	.....	.....	.....	.....
01.AE.CM.11.1156.26	.....	.....	.....	.....	.....	.....	.....
01.AE.CN.12.DE00112CN011	.....	.....	.....	.....	.....	.....	.....
01.AE.HK.04.HK001	.....	.....	.....	.....	.....	.....	.....
01.AE.IR.10.10IR.THR48F	.....	.....	.....	.....	.....	.....	.....
01.AE.IP.11.DE00111JP003	.....	.....	.....	.....	.....	.....	.....
01.AE.SE.11.5E601018	.....	.....	.....	.....	.....	.....	.....
01.AE.TH.10.DE00110TH001	.....	.....	.....	.....	.....	.....	.....
01.AE.TH.90.CM240	.....	.....	.....	.....	.....	.....	.....
01.AE.US.05.306163.FL	.....	.....	.....	.....	.....	.....	.....
01.AG.CM.10.DEM010CM013	.....	.....	.....	.....	.....	.....	.....
02.AG.DE.08.081114	.....	.....	.....	.....	.....	.....	.....
02.AG.GW.05.CC.0048	.....	.....	.....	.....	.....	.....	.....

Table of HIV-1 protein sequences including glycosylation NGS, glycosylation NNT, glycosylation NKT, and CD4 binding sites. The table lists various protein segments with their amino acid sequences and associated glycosylation sites.



glycosylation NST  
glycosylation NST

Table with columns for protein IDs, amino acid sequences, and glycosylation sites. Includes sub-headers for glycosylation NST, glycosylation NNT, CD4 binding, glycosylation NIT, glycosylation NES, and fusion peptide. Rows list various HIV-1 protein sequences and their glycosylation patterns.

Continuation of the table from the previous block, showing glycosylation sites and fusion peptide sequences for various HIV-1 proteins. Columns include glycosylation NIT, glycosylation NES, and fusion peptide.





	transmembrane domain	gp41 cytoplasmic tail start	glycosylation	NGS	glycosylation NAT	
B.FR.83.HXB2	.....	.....	.....	.....	.....	822
A1.CM.08.886.24	.....	.....	.....	.....	.....	816
A1.CY.08.CY236	.....	.....	.....	.....	.....	828
A1.KE.11.DEM111KE002	.....	.....	.....	.....	.....	829
A1.NG.10.10NG040248	.....	.....	.....	.....	.....	820
A1.PK.14.DEM1114PK001	.....	.....	.....	.....	.....	825
A1.RW.11.DEM111RW002	.....	.....	.....	.....	.....	837
A1.UG.11.DEM110UG009	.....	.....	.....	.....	.....	820
A1.ZA.04.503.15344.T10.A1	.....	.....	.....	.....	.....	831
A2.CM.01.01CM.1445MV	.....	.....	.....	.....	.....	828
A3.SN.01.DD1579	.....	.....	.....	.....	.....	816
A4.CD.97.97CD.KCC2	.....	.....	.....	.....	.....	828
A6.BY.13.PV85	.....	.....	.....	.....	.....	830
A6.CY.09.CY255	.....	.....	.....	.....	.....	821
A6.RU.11.1RU06950	.....	.....	.....	.....	.....	828
A6.UA.12.DEM112UA014	.....	.....	.....	.....	.....	826
B.BR.10.10BR.RJ032	.....	.....	.....	.....	.....	838
B.CA.07.502.1191.03	.....	.....	.....	.....	.....	828
B.CH.08.M2.0803101.NFLG8	.....	.....	.....	.....	.....	851
B.CN.12.DEMB12CN006	.....	.....	.....	.....	.....	828
B.CU.14.14CU005	.....	.....	.....	.....	.....	820
B.DE.13.366396	.....	.....	.....	.....	.....	800
B.ES.14.ARP11495	.....	.....	.....	.....	.....	830
B.FR.11.DEMB11FR001	.....	.....	.....	.....	.....	806
B.HT.05.05HT.129389	.....	.....	.....	.....	.....	828
B.JP.12.DEMB12JP001	.....	.....	.....	.....	.....	830
B.KR.07.HP.18.07JHS10.3909	.....	.....	.....	.....	.....	823
B.RU.11.1RU0211	.....	.....	.....	.....	.....	808
B.SE.12.SEG00057	.....	.....	.....	.....	.....	829
B.TH.10.DEMB10TH002	.....	.....	.....	.....	.....	832
B.US.16.2609	.....	.....	.....	.....	.....	819
C.BR.11.DEM11BR035	.....	.....	.....	.....	.....	834
C.CN.10.YNFL19	.....	.....	.....	.....	.....	834
C.DE.10.622166	.....	.....	.....	.....	.....	821
C.DE.14.ARP11498	.....	.....	.....	.....	.....	806
C.ET.08.ET104	.....	.....	.....	.....	.....	803
C.IN.15.NIRT008	.....	.....	.....	.....	.....	808
C.MW.09.703010256.CH256.w96	.....	.....	.....	.....	.....	819
C.NG.10.10NG020523	.....	.....	.....	.....	.....	834
C.NP.11.11NP016	.....	.....	.....	.....	.....	822
C.PK.14.DEM14PK009	.....	.....	.....	.....	.....	820
C.SE.13.SEG000311	.....	.....	.....	.....	.....	811
C.TZ.08.707010457.CH457.w8	.....	.....	.....	.....	.....	811
C.US.11.17TB4.4G8	.....	.....	.....	.....	.....	820
C.ZA.13.DEM113ZA152	.....	.....	.....	.....	.....	833
C.ZM.14.DEM11ZM006	.....	.....	.....	.....	.....	829
D.BR.10.10BR.RJ108	.....	.....	.....	.....	.....	838
D.CD.03.LA17MuBo	.....	.....	.....	.....	.....	834
D.CM.10.DEMD10CM009	.....	.....	.....	.....	.....	810
D.CY.06.CY163	.....	.....	.....	.....	.....	824
D.KE.11.DEMD11KE003	.....	.....	.....	.....	.....	816
D.KR.04.04KR048	.....	.....	.....	.....	.....	817
D.Z.01.288	.....	.....	.....	.....	.....	818
D.UG.10.DEMD10UG004	.....	.....	.....	.....	.....	813
D.UG.11.DEMD11UG003	.....	.....	.....	.....	.....	823
D.YE.02.02YE516	.....	.....	.....	.....	.....	812
F1.A0.06.A0.06.ANG32	.....	.....	.....	.....	.....	806
F1.AR.02.ARE933	.....	.....	.....	.....	.....	811
F1.BR.10.10BR.RJ015	.....	.....	.....	.....	.....	810
F1.FR.11.DEMF11BR037	.....	.....	.....	.....	.....	821
F1.CY.08.CY222	.....	.....	.....	.....	.....	810
F1.ES.02.ES.X845.4	.....	.....	.....	.....	.....	808
F1.ES.11.VA0053.nfl	.....	.....	.....	.....	.....	812
F1.FR.04.LA221.eRe	.....	.....	.....	.....	.....	808
F1.R0.03.LA20DUC1	.....	.....	.....	.....	.....	829
F1.RU.08.D88.845	.....	.....	.....	.....	.....	828
F2.CM.02.02CM.0016BBY	.....	.....	.....	.....	.....	811
F2.CM.10.DEMF210CM007	.....	.....	.....	.....	.....	813
F2.CM.11.DEURF11CM026	.....	.....	.....	.....	.....	822
G.CD.03.LA23L1Ed	.....	.....	.....	.....	.....	804
G.CM.08.709.10	.....	.....	.....	.....	.....	813
G.CM.10.DEMG10CM008	.....	.....	.....	.....	.....	813
G.CM.10.DEURF10CM020	.....	.....	.....	.....	.....	839
G.CN.08.GX.2084.08	.....	.....	.....	.....	.....	825
G.ES.14.ARP1201	.....	.....	.....	.....	.....	844
G.GH.03.03GH175G	.....	.....	.....	.....	.....	824
G.KE.08.LAS.mMe	.....	.....	.....	.....	.....	822
G.KE.09.DEMG09KE001	.....	.....	.....	.....	.....	818
G.NG.12.12NG060409	.....	.....	.....	.....	.....	837
H.CD.04.LA19KoSa	.....	.....	.....	.....	.....	825
H.CF.02.LA25LeM1	.....	.....	.....	.....	.....	813
H.GB.00.00GBAC4001	.....	.....	.....	.....	.....	818
J.CD.03.LA26D1An	.....	.....	.....	.....	.....	831
J.CD.07.1.97CD.KTB147	.....	.....	.....	.....	.....	839
J.SE.93.SEG280.7887	.....	.....	.....	.....	.....	814
K.CD.97.97ZR.EQT111	.....	.....	.....	.....	.....	817
K.CM.96.96CM.MP535	.....	.....	.....	.....	.....	808
01.AE.AF.07.569M	.....	.....	.....	.....	.....	824
01.AE.CM.11.1156.26	.....	.....	.....	.....	.....	815
01.AE.CN.12.DE00112CN011	.....	.....	.....	.....	.....	832
01.AE.HK.04.HK001	.....	.....	.....	.....	.....	825
01.AE.IR.10.10IR.THR48F	.....	.....	.....	.....	.....	833
01.AE.IP.11.DE00111JP003	.....	.....	.....	.....	.....	822
01.AE.SE.11.SEG01018	.....	.....	.....	.....	.....	818
01.AE.TH.10.DE00110TH001	.....	.....	.....	.....	.....	830
01.AE.TH.90.CM240	.....	.....	.....	.....	.....	822
01.AE.US.05.306163.FL	.....	.....	.....	.....	.....	802
02.AG.CM.10.DEM0210CM013	.....	.....	.....	.....	.....	816
02.AG.DE.10.101114	.....	.....	.....	.....	.....	841
02.AG.GW.05.CC.0048	.....	.....	.....	.....	.....	833

Accession	transmembrane domain		gp41 cytoplasmic tail start	glycosylation NGS		glycosylation NAT	
	Start	End	Start	Start	End	Start	End
B. FR. 83. HBX2							
02 AG. KR. 12. 12MHI11 10746	02	AG. KR. 12. 12MHI11	10746	KWASLWNFNITNWLWYKLFIMIVGGLVGLRIFVAVLSIVNVRQGYSPLSFQTHL. PT. PR. GPDREGIEEEGGERDRDRSRLVNGSLALIWDDLSRLCFLSYHRLRDLILLIVTRIVELLGRR. . . . .	GWEALKYWNMLQYV. SQELKNSAVSLLNATAIAV. . . . .		
02 AG. KR. 12. 12MHR9	02	AG. KR. 12. 12MHR9					
02 AG. LR. x. POC44951	02	AG. LR. x. POC44951					
02 AG. NG. 12. 12NG066418	02	AG. NG. 12. 12NG066418					
02 AG. NE. x. IBS0	02	AG. NE. x. IBS0					
02 AG. SE. x. IFE602024	02	AG. SE. x. IFE602024					
02 AG. SN. 13. 9580	02	AG. SN. 13. 9580					
03 AB. RU. 97. KAL153 2	03	AB. RU. 97. KAL153 2					
04 cpx. CY. 94. 94CY032 3	04	cpx. CY. 94. 94CY032 3					
05 OF. BE. x. VT110	05	OF. BE. x. VT110					
06 cpx. AU. 96. BFP90	06	cpx. AU. 96. BFP90					
07 BC. CN. 98. 98CN009	07	BC. CN. 98. 98CN009					
08 BC. CN. 97. 97CNX 6F	08	BC. CN. 97. 97CNX 6F					
09 cpx. GH. 96. 96GH2911	09	cpx. GH. 96. 96GH2911					
10 CD. TZ. 96. 96TZ BF061	10	CD. TZ. 96. 96TZ BF061					
11 cpx. CM. 95. 95CM 1816	11	cpx. CM. 95. 95CM 1816					
12 BF. AR. 99. ARMA159	12	BF. AR. 99. ARMA159					
13 cpx. CM. 96. 96CM 1849	13	cpx. CM. 96. 96CM 1849					
14 BG. ES. 05. X1870	14	BG. ES. 05. X1870					
15 01B. TH. 99. 99TH MU2079	15	01B. TH. 99. 99TH MU2079					
16 AZD. FR. 97. 97FR001	16	AZD. FR. 97. 97FR001					
17 BF. AR. 99. ARMA038	17	BF. AR. 99. ARMA038					
18 cpx. CU. 99. CU76	18	cpx. CU. 99. CU76					
19 cpx. CU. 99. CU7	19	cpx. CU. 99. CU7					
20 BG. CU. 99. CU103	20	BG. CU. 99. CU103					
21 AZD. KE. 99. KER2003	21	AZD. KE. 99. KER2003					
22 01A1. CM. 01. 01CM 0001BBY	22	01A1. CM. 01. 01CM 0001BBY					
23 BG. CU. 03. CB118	23	BG. CU. 03. CB118					
24 BG. ES. 08. X2456 2	24	BG. ES. 08. X2456 2					
25 cpx. CM. 02. 1918E	25	cpx. CM. 02. 1918E					
26 AU. CD. 02. 02CD MBT0047	26	AU. CD. 02. 02CD MBT0047					
27 cpx. FR. 04. 04FR patient K25	27	cpx. FR. 04. 04FR patient K25					
28 BF. BR. 99. BREPM12609	28	BF. BR. 99. BREPM12609					
29 BF. BR. 01. BREPM16704	29	BF. BR. 01. BREPM16704					
31 BC. BR. 04. 04BR142	31	BC. BR. 04. 04BR142					
32 06A1. EE. 01. EE0369	32	06A1. EE. 01. EE0369					
33 01B. ID. 07. JKT189 C	33	01B. ID. 07. JKT189 C					
34 01B. TH. 99. 01BTH1969P	34	01B. TH. 99. 01BTH1969P					
35 AD. AF. 07. 169H	35	AD. AF. 07. 169H					
36 cpx. CM. 00. 00CMNYU030	36	cpx. CM. 00. 00CMNYU030					
37 cpx. CM. 00. 00CMNYU826	37	cpx. CM. 00. 00CMNYU826					
38 BFI. UY. 03. UY03 3389	38	BFI. UY. 03. UY03 3389					
39 BF. BR. 04. 04BRR3179	39	BF. BR. 04. 04BRR3179					
40 BF. BR. 05. 05BRR1055	40	BF. BR. 05. 05BRR1055					
42 BF. LU. 03. LuBF 01 03	42	BF. LU. 03. LuBF 01 03					
43 02G. SA. 03. J11223	43	02G. SA. 03. J11223					
44 BF. CL. 00. CH80	44	BF. CL. 00. CH80					
45 cpx. FR. 04. 04FR AUK	45	cpx. FR. 04. 04FR AUK					
46 BF. BR. 07. 07BR FPS625	46	BF. BR. 07. 07BR FPS625					
47 BF. ES. 08. P1942	47	BF. ES. 08. P1942					
48 01B. MY. 07. 07MYKT021	48	01B. MY. 07. 07MYKT021					
49 cpx. GM. 03. N26677	49	cpx. GM. 03. N26677					
50 A1D. GB. 10. 12792	50	A1D. GB. 10. 12792					
51 01B. SG. 10. 125G HM021	51	01B. SG. 10. 125G HM021					
52 01B. MY. 03. 03MYK1018 1	52	01B. MY. 03. 03MYK1018 1					
53 01B. MY. 11. 11FIR164	53	01B. MY. 11. 11FIR164					
54 01B. MY. 09. 09MYSB023	54	01B. MY. 09. 09MYSB023					
55 01B. CN. 10. HNC5102056	55	01B. CN. 10. HNC5102056					
56 cpx. FR. 10. 10UG patient A	56	cpx. FR. 10. 10UG patient A					
57 BC. CN. 09. 09BNC1959	57	BC. CN. 09. 09BNC1959					
58 01B. MY. 09. 09MYPR37	58	01B. MY. 09. 09MYPR37					
59 01B. CN. 09. 09LNA423	59	01B. CN. 09. 09LNA423					
60 BC. IT. 11. BAV499	60	BC. IT. 11. BAV499					
61 BC. CN. 10. J1100010	61	BC. CN. 10. J1100010					
62 BC. CN. 10. YNFL13	62	BC. CN. 10. YNFL13					
63 02A1. RU. 10. 10RU6637	63	02A1. RU. 10. 10RU6637					
64 BC. CN. 09. YNFL31	64	BC. CN. 09. YNFL31					
65 cpx. CN. 10. YNFL01	65	cpx. CN. 10. YNFL01					
67 01B. CN. 11. ANHUI HF115	67	01B. CN. 11. ANHUI HF115					
68 01B. CN. 11. ANHUI WH73	68	01B. CN. 11. ANHUI WH73					
69 01B. JP. 05. 05JPMYC1135P420	69	01B. JP. 05. 05JPMYC1135P420					
70 BFI. BR. 10. 10BR PE004	70	BFI. BR. 10. 10BR PE004					
71 BFI. BR. 10. 10BR PE008	71	BFI. BR. 10. 10BR PE008					
72 BFI. BR. 10. 10BR MG002	72	BFI. BR. 10. 10BR MG002					
73 BG. DE. 01. U96 01	73	BG. DE. 01. U96 01					
74 01B. MY. 10. 10MYPR268	74	01B. MY. 10. 10MYPR268					
78 cpx. CN. 13. YNCT19	78	cpx. CN. 13. YNCT19					
85 BC. CN. 14. 14CN SCYB2	85	BC. CN. 14. 14CN SCYB2					
86 BC. CN. 13. 15YHNS18	86	BC. CN. 13. 15YHNS18					
87 cpx. CN. 12. DH32	87	cpx. CN. 12. DH32					
88 BC. CN. 05. 05YHNL259g	88	BC. CN. 05. 05YHNL259g					
0. CM. 96. LA51YBF35	0.	CM. 96. LA51YBF35					
0. CM. 96. LA52YBF39	0.	CM. 96. LA52YBF39					
0. CM. 99. CMU4122	0.	CM. 99. CMU4122					
0. CM. x. pCM02 3	0.	CM. x. pCM02 3					
0. ES. 01. Rea215 HIV Group0	0.	ES. 01. Rea215 HIV Group0					
0. FR. 06. LA55RBF206	0.	FR. 06. LA55RBF206					
0. GA. 11. 11GAb6352	0.	GA. 11. 11GAb6352					
0. SN. 99. 99SE MP1299	0.	SN. 99. 99SE MP1299					
0. SN. 99. 99SE MP1300	0.	SN. 99. 99SE MP1300					
0. US. 10. LTNP	0.	US. 10. LTNP					
N. CM. 06. U14296	N.	CM. 06. U14296					
N. FR. 99. FR 2011	N.	FR. 99. FR 2011					
P. CM. 06. U14788	P.	CM. 06. U14788					
P. FR. 09. RBF168	P.	FR. 09. RBF168					
CPZ. TZ. 06. TAN5	CPZ.	TZ. 06. TAN5					
CPZ. US. 85. US Marilyn	CPZ.	US. 85. US Marilyn					
GOR. CM. 12. SIVgor_BPID2	GOR.	CM. 12. SIVgor_BPID2					
GOR. CM. 13. SIVgor_BPID15	GOR.	CM. 13. SIVgor_BPID15					

Env end  
gp41 end  
cytoplasmic tail end  
..... AEGTDRVIEVVOGA<sup>\*</sup>CAIRHIPPRI<sup>\*</sup>RQGLERILL<sup>\*</sup>  
A1.CM.08.886 24 ..... -GW- W- LG-RI- -N- -A-  
A1.CY.08.CY236 ..... -GW- -I- -IG- IN- -A-  
A1.KE.11.DEMA111KE002 ..... -GW- -A- LG-RF- -L- -A-  
A1.NG.10.10NG040248 ..... -GW- -A- IGRRI- -LN- -A-  
A1.PK.14.DEMA114PK001 ..... -GW- W- NGG-RTV- -FLN- -A-  
A1.RW.11.DEMA111RW002 ..... -GW- -I- -RT- -LN- T- F-A-  
A1.UG.11.DEMA110UG009 ..... -GW- -I- -IG-RIG- -LNV- T- -A-  
A1.ZA.04.503 15344 T10\_A1 ..... -GW- -IG- RVG- -LN- T- F-A-  
A2.CM.01.01CM 1445MV ..... -GW- -LG-RI- -LN- T- F-A-  
A3.SN.01.DD1579 ..... -W- -IG- R-G- -LL- -V- -A-  
A4.CD.97.97CD\_KCC2 ..... -W- -A- -G-RIG- -FLN- -F- -A-  
A6.BY.13.PV85 ..... -G- -I- -I- -RX- -CN- -A- -A- Q-  
A6.CY.09.CY255 ..... -GW- -IG- RLG- -CN- -A- -A- Q-  
A6.RU.11.11RU06950 ..... -GW- -IG- -CN- -A- -A- Q-  
A6.UA.12.DEMA112UA014 ..... -GC- -RFF- -L- -N- -A- -IA- Q-  
B.BR.10.10BR\_RJ032 ..... -I- -IA- RIG- G- -L- -T- -A-  
B.CA.07.502 1191 03 ..... -I- -L- R-G- -VL- V- -F- -S-  
B.CH.08.M2 0803101 NFLG8 ..... -I- -LA- RGF- -FL- -A- -Q-  
B.CN.12.DEMB12CN006 ..... -V- -A- AIG- -FLN- -A- -IA- Q-  
B.CU.14.14CU005 ..... -I- -I- -R- -FL- -F- -L-  
B.DE.13.366396 ..... -I- -G- RIG- G- -L- -A- -Q-  
B.ES.14.ARP1195 ..... -I- -A- RFF- G- -L- -A-  
B.FR.11.DEMB11FR001 ..... -I- -RT- -I- -V- -A-  
B.HT.05.05HT 129389 ..... G- -I- -I- -RRVV- -L- V- T- -A-  
B.JP.12.DEMB12JP001 ..... -I- -I- -RL- -L- -V- -A-  
B.KR.07.HP 18 07JHS10 3909 ..... -G- -A- IL- R-Y- -L- -V- -A-  
B.RU.11.11RU021 ..... -G- -RT- F- -VL- -F- -A-  
B.SE.12.SEG00057 ..... -K- -I- -RT- -A- -A-  
B.TH.10.DEMB10TH002 ..... -G- -#- -A- -E- -A- -Q-  
B.US.16.2609 ..... G- -I- -L- RFG- G- -L- -A-  
C.BR.11.DEMC11BR035 ..... -I- -I- -IW- -CN- -F- -AA- Q-  
C.CN.10.YNFI19 ..... -I- -AIX- R- W- -T- -G- D- P- VA- Q-  
C.DE.10.622166 ..... -I- -A- TI- -F- -N- -F- -A-  
C.ES.14.ARP1198 ..... -I- -GSI- RT- -LN- -F- -AT-  
C.ET.08.ET104 ..... V- R- TGIM- L- -K- W- DFO- -I- -F- -SFP-  
C.IN.15.NIRT008 ..... -IL- AI- RIWT- -N- -A- -IA- Q-  
C.MW.09.703010256 CH256.w96 ..... -I- -FL- RI- -Y- -F- -AA- Q-  
C.NG.10.10NG020523 ..... -IL- -ILRF- -N- T- -F- -AA-  
C.NP.11.11NP016 ..... -I- -RT- -F- -N- -Q-  
C.PK.14.DEMC14PK009 ..... G- -F- LI- NIY- -N- V- -AS-  
C.SE.13.SEG000311 ..... VKPE- -FMKLF- RVG- V- SN- L- ELS- -IVFQ-  
C.TZ.08.707010457 CH457.w8 ..... -I- -L- -RI- -CNV- T- -AA- Q-  
C.US.11.17TB4 4G8 ..... -I- -FL- RTW- -CNV- -F- -AA-  
C.ZA.13.DEMC13ZA152 ..... -I- -FI- RF- -CNV- T- -F- -AA- Q-  
C.ZM.11.DEMC11ZM006 ..... -I- -L- LNI- -LS- -F- -AA- Q-  
D.BR.10.10BR\_RJ108 ..... -L- RIG- -IN- -F- -A-  
D.CD.03.LA17MuBo ..... -I- -R- -VL- -F- -A-  
D.CM.10.DEMD10CM009 ..... -A- LR- F- -L- -F- -A-  
D.CY.06.CY163 ..... T- -RT- -VLR- -F- -A-  
D.KE.11.DEMD11KE003 ..... L- IGLRIG- -IN- -F- -A-  
D.KR.04.04KBH8 ..... -R- F- -VL- -A- -I-  
D.TZ.01.288 ..... -I- -II- R- F- -VL- -V- -A-  
D.UG.10.DEMD10UG004 ..... -I- -L- RIG- -LN- T- -A- -AF-  
D.UG.11.DEMD11UG003 ..... -L- -R- G- -VLN- -F- -A-  
D.YE.02.02YE516 ..... -I- -I- -R- G- -LN- -A-  
F1.A0.06.A0 06 ANG32 ..... -L- R- G- -VL- -F- -A-  
F1.AR.02.ARE933 ..... -I- -A- R- V- -VCN- -AF-  
F1.BR.10.10BR\_RJ015 ..... G- -I- -AL- RFG- -LN- -F- -A- I-  
F1.BR.11.DEMF11BR037 ..... -A- -ALRR- VT- -LN- -F- -A-  
F1.CY.08.CY222 ..... -AL- R- G- -VLNV- -K- -A-  
F1.ES.02.ES\_X845 4 ..... -I- -AL- RTG- -L- -V- -A-  
F1.ES.11.VA0053 nFl ..... LL- -L- -G- -VLN- -F- -L-  
F1.FR.04.LA22LeRe ..... -R- -IS- RIG- -VLNV- -F- -A-  
F1.R0.03.LA26DuCl ..... -I- -AL- R- G- -VLNA- -A-  
F1.RU.08.D88 845 ..... -W- -L- -AL- R- G- -VL- -L-  
F2.CM.02.02CM 0016BBY ..... -IL- R- G- -L- -F- -A-  
F2.CM.10.DEMF210CM007 ..... -I- D- L- RIG- -VL- -F- -A-  
F2.CM.11.DEURF11CM026 ..... -IL- GL- RVG- -VL- -F- -A-  
G.CD.03.LA23LiEd ..... -NW- -G- -RI- -FLN- -F- -V-  
G.CM.08.709 10 ..... -N- -I- -G- -RI- -LN- -A-  
G.CM.10.DEMG10CM008 ..... -DW- -A- RVG- -FLN- -F- -A-  
G.CM.10.DEURF10CM020 ..... -NW- -A- RVG- -VLN- -A- -A-  
G.CN.08.GX 2084 08 ..... -NW- -AHR- -CN- -A- -V-  
G.ES.14.ARP1201 ..... -NW- -A- RTG- -LN- -A- -Q-  
G.GH.03.03GH175G ..... -NW- -I- -R- G- -LN- T- -F- -A-  
G.GW.08.LAS7LmNe ..... -N- -A- -LRVG- -FLN- -F- -A-  
G.KE.09.DEMG09KE001 ..... -N- -I- -R- -VL- -F- -SA-  
G.NG.12.12NG060409 ..... -NW- -I- -R- G- -LN- -A-  
H.CD.04.LA19KoSa ..... -I- -IG- RI- -LN- -A-  
H.CF.02.LA25LeMi ..... -I- -I- -R- G- -I- -T-  
H.GB.00.00GBAC4001 ..... -I- -L- R- G- -I- -F- -A-  
J.CD.03.LA26DIAp ..... -I- -R- A- -VLN- -F- IA-  
J.CD.97.J 97DC\_KTB147 ..... -A- -I- -IF- -L- -X- -A-  
J.SE.93.SEG280 7887 ..... -I- -IA- R- F- -L- -A-  
K.CD.97.97ZR\_EQTb11 ..... -I- -I- YP- F- LL- -F- -L-  
K.CM.96.96CM\_MP535 ..... -G- -I- -IG- R- F- -LL- -F- -A-  
01.AE.AF.07.569M ..... -GW- -I- -W- FI- -F- -A-  
01.AE.CM.11.1156 26 ..... -GW- -F- I- -R- -VL- -F- -A-  
01.AE.CN.12.DE00112CN011 ..... -W- -I- -AA- R- G- -L- -A- -Q-  
01.AE.HK.04.HK001 ..... -W- -A- R- W- -L- -T- V-  
01.AE.IR.10.10IR\_THR48F ..... -GW- -A- R- W- -LL- -A-  
01.AE.JP.11.DE00111JP003 ..... -GW- -A- W- -L- -T- -A-  
01.AE.SE.11.SEG01018 ..... -GW- -LA- T- W- T- L- -R- -HV-  
01.AE.TH.10.DE00110TH001 ..... -GW- -I- -A- -W- -L- -A-  
01.AE.TH.90.CM240 ..... -GW- -A- -W- -L- -T-  
01.AE.US.05.306163 FL ..... -W- -A- RTG- -LN- -A- I-  
02.AG.CM.10.DE00210CM013 ..... -NW- -I- -R- -Y- -N- -A-  
02.AG.DE.10.701114 ..... G.NW- -I- -IG- ATG- -N- -A-  
02.AG.GW.05.CC\_0048 ..... -NW- -I- -IG- S- -CN- T- -L- -A-

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	myristoylation	Nef start				acidic cluster	phosphorylation		
							poly-P helix		
B.FR.83.HXB2	MGGKWSKSS.VIGWPTVRRMR	AE	PAADRVAASR		DLEKHAITSNTAATNAACAWLEA	QE	E.E.EVGFVPTQVPLRPMYKAAVDLSHFLKGGLEGLHSORRQDILDLDWIYHTQGYF		121
A1.CM.08.886.24	IV-OI-L-Q	S	EG-KV-Q		D-V-I-I.NHPSV	K	D-R	L-TY-RK	V-N-F
A1.CY.08.CY236	IV-EI-I-Q	TP	A-SG-V-Q		D-V-X			D-Y-K	119
A1.KE.11.DEMA111KE002	IV-EI-I-Q	TP	S-PG-V-Q		D-V-L.NHPS	V	G-R	G-F-D-Y-KK	E-V-F
A1.NG.10.10NG040248	Q-R-R.MP	SEI	TPPGER	OTP	TG-V-Q			D-V-K	129
A1.PK.14.DEMA114PK001	N-R-K.VE	E-D	A	TPP	TA-TG-V-Q		E.D.G	R-G-L	D-MY-KK
A1.RW.11.DEMA111RW002	S-IV-E-I-Q	TP	RRA	TPP	AG-V-Q			F-G-F	D-Y-K
A1.UG.11.DEMA110UG009	IV-EI-I-Q	TP	A-TG-V-Q		R-I.NHPS	V	D-R	F-F	D-Y-RK
A1.ZA.04.503.15344.T10.A1	IV-AI-I-Q	TP	TPTAAR	QTPT	IG-V-Q			G-L	VY-RK
A2.CM.01.01CM.1445MV	S-L	A	TP	A	IG-V-Q			G-F	D-Y-K
A3.SN.01.DDI579	R.QE	HK-D-Q	TPP	T	EG-V-Q			S-V-T-Q	AS-S-T
A4.CD.97.97CD.KCC2	LV-A-D	Q	TP	A	EG-V-Q			D-Y-V-N	PD
A6.BY.13.PV85	IV-OI	I	PAP	APE	TG-PV-Q			D-V	XX-D
A6.CY.09.CY255	CG.IV	SO-I	P	PA	SG-PV-Q			D-V	X
A6.RU.11.1RU6950	R.IV	O-I	PA	PA	SG-PV-Q			DR-V	R
A6.UA.12.DEMA112UA014	R.KAE	O-Q	P	A	IG-PV-Q			A-V	R-D
B.BR.10.10BR.RJ032	R.MG	N-D	TPPTE	SAAE	IG-V			R-V	D
B.CA.07.502.1191.03	GG.MG	NA-D	T		EG			R	N-PD
B.CH.08.M2.0803101.NFLG8	S-L	C-PV-S-I	T	PRNE	ONEQ	VG		R	N
B.CN.12.DEMB12CN006	W	DA-I	T		EG			AER	T-EN
B.CU.14.14CU005	L-RI	G-A	T		EG			Q	L-N
B.DE.13.366396	V	A		PA	AE	V		Y	N-D
B.ES.14.ARP1495	LS	A		PA	AE	V		R	V-TTN
B.FR.11.DEMB11FR001	IF-R	GG-A	TGTFPKAERLGRKVRTE	EG	V			R	T
B.HT.05.05HT.129389	A	R-AI	P	AAE	G	V		R	L-T
B.JP.12.DEMB12JP001	IV-A	I	P	RAE	EG	V		R	T
B.KR.07.HP.18.07JHS10.3909	R	P-DAI	T		EG	V		QR	T-SN
B.RU.11.11RU21R	L-RI	I-Q	T		EG	V			
B.SE.12.SEG00057	R	AA-AI	Q	T		EG			
B.TH.10.DEMB10TH002	S	LG	OP	AO	G				N-PDS
B.US.16.2609	LG	SN	PAT	DGEG	VSODR	V			N
C.BR.11.DEMC11BR035	S	C-LV-N	G		EG	P-Q		DRY	L-P-N
C.CN.10.YNFL19	A	IV-AI	T		EG	V-Q			I-N-D
C.DE.10.622166	N	R-IV-AI	GP	RAE	EG	Q			L-T
C.ES.14.ARP1498	N	IV-AI	TP		EG	Q			L-T
C.ET.08.ET104	M	C-PV-C-I-Q	NDP	ROPE	VG	Q			P
C.IN.15.NIRT008	QC	IV-A-L	T		EG	Q			P
C.MW.09.703010256.CH256.W96	IV	N-I	TD		EG	Q			L-T
C.NG.10.10NG0820523	IV	D-I	TAP		EG	Q			L-T
C.NP.11.11NP11R	IV	A-D	T		EG	Q			L-T
C.PK.14.DEMC14PK009	Q	A	RP	E	EG	Q			L-T
C.SE.13.SEG000311	SS	CI-PV-CLV	ISO	II	PPEG	FG			PLP-T
C.TZ.08.707010457.CH457.W8	C	MV-E	I	TA		EG			P
C.US.11.17TB4.4G8	SA	C-PR-AI	I	APAAEGIR	RAA	EG	V		L-T
C.ZA.13.DEMB13ZA152	N	IV-AI	QA	SPATEG	EG	Q			L-T
C.ZM.14.DEMC14ZM006	N	IV-AI	I		EG	Q			L-T
D.BR.10.10BR.RJ108	IV	A-I	T		G	V			S
D.CD.03.LA17MuBo	G	LC-A-I	TD		G	V			T
D.CM.10.DEMD10CM009	IV	AI	TOP	TE	G	V			Q-D
D.CY.06.CY163	IV	AI-IK	TD		G	V			X
D.KE.11.DEMD11KE003	IV	AI-I	T		AG	V			SQ-D
D.KR.04.04KR04	IV	AI-I	T		G	V			R
D.LZ.01.LZ88	IV	AI-I	T		G	V			R
D.UG.10.DEMD10UG004	IV	AI-I	TD		EG	K			H-D
D.UG.11.DEMD11UG003	IV	AI-I	TA		EG	K			Q-S
D.YE.02.02YE516	IV	I-KI-K	TD		G	V			N-P
F1.A0.06.A0.06.ANG32	IV	AI	TP	A	EG	V-Q			IN-R
F1.AR.02.ARE933	IV	EI	TP		EG	V-Q			KNR-PDL
F1.BR.10.10BR.RJ015	NK	IP-AI	PPAE	RMGA	EG	Q			RD-PDV
F1.BR.11.DEMF11BR037	IV	AI-Q	TPPAERARR	GQNP	EG	Q			STN-PEL
F1.CY.08.CY222	C	IV-A	TP		EG	V-Q			V-X
F1.ES.02.ES.X845.4	IV	A-D	TP	A	EG	V-Q			S
F1.ES.11.VA0053.nf1	IV	A	TPPAAEV	GRTP	EG	V-Q			T-S-N
F1.FR.04.LA221Re	IV	A	P		EG	V-Q			R-S-N
F1.R0.03.LA26DUC1	N	IV-A-I	TPPAA	EGVE	EG	V-Q			R-S-PDL
F1.RU.08.D88.845	A	IV-AI-D	PPAA	PPAAEGX	EG	V			R-PDL
F2.CM.02.02CM.0016BBY	IV	K-Q	TP	V	EG	KV-Q			G-MDI
F2.CM.10.DEMF210CM007	IV	I-IKO	TP	V	EG	V-Q			Y-KE-PDL
F2.CM.11.DEURF11CM026	R	IV-A-I-Q	TPVA	EEG	EG	V-Q			R-RD-PDL
G.CD.03.LA231Ed	R	RV-SA-I	TPP	NP	EG	V-Q			V-TN
G.CM.08.709.10	R	IV-E	L-Q	PPG	OTPO	AG	V-Q		I-N-D
G.CM.10.DEMG10CM008	L	RR-MP-EI-L	TP	T	EG	Q			S-PD
G.CM.10.DEURF10CM020	C	IV-EI-I-Q	TP		EG	Q			S-PD
G.E.S.14.ARP1201	N	KS-KI-Q	TPPAA	EGVE	EG	Q			S-PD
G.GH.03.03GH1K6	I	R-IKE	K-QI-Q	A	EG	Q			L-EN
G.GH.08.LAS71m6	C	IV-KI-Q	TP	A	EG	Q			L-N
G.KE.09.DEMG09KE001	N	C-V-Q	I	TPPAAEGE	AAASP	EG	Q		TN-PD
G.NG.12.12NG060409	N	NK-IV-EI-Q	TP	A	EG	Q			Q-PD
H.CD.04.LA19KoSa	MV	A			EG	Q			IN
H.CF.02.LA25LeM1	N	IV-S			EG	V			V-IN
H.GB.00.00GBAC4001	R	IV-RI-I			EG	PV			V-IN
J.CD.03.LA26D1An	SS	NK-RE-SOI	APA	AA	G	V-Q			V-N
J.CD.07.J.97CD.KTB147	N	IV-SEI	TP	DA	EG	Q			VE-S
J.SE.93.SEG280.7887	N	IV-Q	I	P		EG	Q		S
K.CD.97.97ZR.EOTB11	IV	S-K	TP		G	V-Q			V-SH
K.CM.96.96CM.MP535	IV	AI	TP	RPAADR	GTQ	G	V-Q		SHN-PD
01.AE.AF.07.569N	S	IV-Q	KIKK	TP	EG	V-Q			M-N
01.AE.CM.11.1156.26	IV	Q	IKO	TP	V	EG	V-K		I-SS-S
01.AE.CN.12.DE0012CN011	IV	Q	IKO	TP	T	EG	V-Q		I-N
01.AE.HK.04.HK001	IV	Q	I-Q	TP	TEG	V-Q			N-N
01.AE.IR.10.10IR.THR48F	S	IV-Q	I-Q	TP	TEG	V-Q			N-N
01.AE.JP.11.DE0011JP003	C	IV-MG	TI-I-Q	TP	EG	V-Q			M-N
01.AE.SE.11.SEG01018	C	IV-SQ	I-Q	TP	EG	V-Q			M-N
01.AE.TH.10.DE0010TH001	GT	KG-RQ	KIEQ	TP	EG	V-Q			M-N
01.AE.TH.90.CM240	S	IV-Q	KIKO	TP	TEG	V-Q			M-N
01.AE.US.05.306163.FL	IV	O-I	I	TP	TEG	V-Q			M-N
02.AG.CM.10.DEMD10CM013	IV	Q	I-H	TPARGERAG	GEAP	EG	Q		S-PV
02.AG.DE.09.081114	N	RV-TR	KIAQ	TPPTPD	P	TGI	Q		H-D
02.AG.GW.05.CC.0048	IV	Q	I-KO	TP	EG	Q			L-E

	myristoylation	Nef start		acidic cluster	phosphorylation	poly-P helix
B. FR. 83. HXB2	MGGKWSKSS. VIGWPTVRRMR	AE	PAADRVAASR	DLEKHGAIITSNTAATNAACAWLEA	QE	E. E. EVGFPVTPQVPLRPMYKAAVDLSHFLKKEGGLEGLHSORRQDILDWLHYHTQGYF
02 AG. KR. 12. 12MHI11 10746	IV-K-I-Q	TP	IG-Q	DR-D-PD	E	T-K-G-L-VY-KK-E-V
02 AG. KR. 12. 12MHR9	IV-R-L	TPPAAEAGV	AASTP-EG-Q	DRR-RR	E	EG-R-G-F-R-Y-KK-E-V
02 AG. LR. x. POC44951	LV-K-I-Q	TPVSE	R-KG-V-Q	DRR-DR	GS-D	R-G-L-D-K-E-V-N
02 AG. NG. 12. 12NG066418	N	TPAR	ONP-TG-Q	DR-L-T	S-ED	D-Y-KK-E-V-N
02 AG. NG. x. 1B90	IV-K-NK-Q	TP	TG-Q	DR-T	Q-PD	R-D-Y-KK-E-V-N
02 AG. SE. x. E6G02024	TV-SRI-L	TPV	ROT-TG-Q	DR-T	RS-V	E-D-N-G-F-D-Y-KK-E-V
02 AG. SN. 13. 9580	IV-K-I-Q	PAP	VPSA-PG-Q	DR-#S	ST-D	R-N-N-VY-KK-E-V
03 AB. RU. 97. KAL153 2	IV-Q-I	P	A-R-PV-Q	D-Y-V	N-D	R-G-F-N-D-Y-KK-E-V
04 cpx. CY. 94. 94CY032 3	IV-EI	RAEPPERMR	RAQAE-AG-V-Q	D-NR-V	IN-PDKT	E-F-G-L-D-Y-KK-E-V
05 cpx. BE. x. VT110	N	TPPT	ER-EG-V-Q	DRN-V	IR-V	PDH-V-E-K-R-V-F-F-D-Y-KK-E-V-N
06 cpx. AU. 96. BFP90	IV-DI	T	EO-G-V-Q	D	GE-V	T-E-K-R-V-F-F-D-Y-KK-E-V
07 BC. CN. 98. 98CN009	IV-AI	I	T-G-V	DR-L	D-D	T-E-K-R-V-F-G-F-F-D-Y-KK-E-V
08 BC. CN. 97. 97CNGX 6F	X	IV-EI	I-TSP-EG-Q	GR-L	S-HD	E-D-D-R-G-F-F-D-Y-KK-E-V
09 cpx. GH. 96. 96GH2911	IV-EI	I-TS	EG-Q	A-F	L-PGN	D-A-D-R-F-G-F-GF-D-Y-KK-E-V
10 CD. TZ. 96. 96TZ BF061	R	IV-EI	I-TSPT-EG-Q	NR	R-N-P-L	E-F-G-F-GF-D-Y-KK-E-V
12 BF. AR. 99. ARMA159	IV-EI	L-TP	EG-V-Q	DR-V	L-KDYV	E-G-S-K-R-F-G-F-GF-D-KK-E-V
13 cpx. CM. 96. 96CM 1849	R	IV-EI	L-SP-EG-V-Q	DR-V	L-N-PD	OE-D-S-R-F-G-F-GF-D-Y-KK-E-V
14 BG. ES. 05. X1870	S	IV-Q	KIKO-TP-EG-V-Q	DN-V	M-N	DSV-R-E-D-S-R-F-F-F-D-Y-KK-E-V
15 01B. TH. 99. 99TH MU2079	R	LP-A	TPPAAER	RR-V	IN-SN	PDL-E-D-S-R-G-L-R-D-Y-KK-E-V
16 AZD. KR. 97. 97KR000	IV-EI	I-TQ	ELPRTTP-EG-Q	EER	SG-N-S	PTHGR-E-E-G-F-F-D-FF-K-PE-VN
17 BF. AR. 99. ARMA038	L	IV-A	I-Q-G-V	R	D	R-E-A-D-R-G-L-F-IVM-K-VN
18 cpx. CU. 99. CU76	N	IV-A	L-TP-AG-V-Q	A	N	PD-E-E-D-S-R-F-F-F-D-Y-KK-E-V
19 cpx. CU. 99. CU7	IV-Q	I-TD	EG-V-Q	D	V	M-NH-S-V-E-D-N-R-G-F-F-D-Y-KK-E-V
20 BG. CU. 99. CU103	IV-Q	I-TD	EG-V-Q	AR	V	M-NH-S-V-E-D-N-R-G-F-F-D-Y-KK-E-V
21 AZD. KE. 99. KER2003	IV-Q	I-TD	EG-V-Q	AR	V	M-NH-S-V-E-D-N-R-G-F-F-D-Y-KK-E-V
22 01A1. CM. 01. 01CM 0001BBY	N	IV-AA	I-Q-PPA-XNP-AG-V-Q	AR	V	M-NH-S-V-E-D-N-R-G-F-F-D-Y-KK-E-V
23 BG. CU. 03. CB118	N	IV-AA	I-Q-PPA-XNP-AG-V-Q	AR	V	M-NH-S-V-E-D-N-R-G-F-F-D-Y-KK-E-V
24 BG. ES. 08. X2456 2	N	IV-SE	R-I-TPLTTRRGASONSARGES-VG-Q	AR	V	M-NH-S-V-E-D-N-R-G-F-F-D-Y-KK-E-V
25 cpx. CM. 02. 021918E	N	RV-EI	I-TPPA-EAAA-EG-Q	A	S-PD	E-E-S-R-G-F-F-D-VW-K-E-V
26 AU. CD. 02. 02CD MBT047	Q	PV-E	K-TP-TG-V-Q	D	V	SE-PD-E-E-S-R-G-F-F-D-Y-KK-E-V
27 cpx. FR. 04. 04FR K25	R	IV-EI	I-K-TP-EG-V-Q	R	Y	MN-HN-D-E-D-S-R-G-L-R-D-WK-E-V
28 BF. BR. 99. BREPM12609	RG	TG-EA	L-TRP-AAE-G-V-Q	R	Y	MN-HN-D-E-D-S-R-G-L-R-D-WK-E-V
29 BF. BR. 01. BREPM16704	C	MS-AA	L-TPG-PAE-EG-Q	Y		
31 BC. BR. 04. 04BR142	N	CI-PV	AI-L-HPAAERIGSE. RVRGAE-EG-P-Q	DR	L-RDN	D-OE-R-G-F-F-D-Y-KK-E-V
32 06A1. EE. 01. EE0369	IV-EI	L-TP	EG-V-Q	DR	L-HPT	D-E-R-G-F-GF-D-Y-KK-E-V
33 01B. ID. 07. JKT189 C	S	C-E	I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
34 01B. TH. 99. 01BR1969P	IV-Q	I-TD	EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
35 AD. AF. 07. 169H	IV-EI	I-KK-E-K-K-Q	A-EG-V-Q	DR	L	IN-NHPS-T-Q-E-N-R-G-F-F-D-Y-KK-E-V
36 cpx. CM. 00. 00CMNYU830	I	QI-D	Q-TP-IG-V-Q	DR	L	TS-DY-E-G-R-G-F-F-D-K-E-V
37 cpx. CM. 00. 00CMNYU926	IV	QI-I	KO-TP-EG-V-Q	A	R	ST-PD-GE-D-P-D-R-G-F-F-D-K-E-V
38 BFI. UY. 03. UY03 3389	RR	IV	ADI-K-AT-D-TPPTAER-GAAG-EG-Q	DRR	L	KDN-PDV-E-N-R-G-L-VW-K-E-V
39 BF. BR. 04. 04BR3179	R	P-EI	D-TPAA-DGER-G-Q	A	L	VSN-D-E-N-R-HR-I-RKE-K-E-V
40 BF. BR. 05. 05BRR055	L	V-A	K-T-TPPTAAE-GAGT-EG-Q	AR	L	T-KD-V-R-R-G-L-F-VY-KK-E-V
42 BF. LU. 03. luBF 01 03	R	MG	SEI-I-TPPTAAE-GAGT-EG-Q	AR	L	T-KD-V-R-R-G-L-F-VY-KK-E-V
43 02G. SA. 03. J11223	C	IV	DI-L-TP-EG-KV-Q	DR	V	S-N-PDV-E-D-R-F-G-F-F-D-Y-KK-E-V
44 BF. CL. 08. CH80	IV	DI	L-TP-EG-V-Q	D	V	R-N-RDN-PDV-E-D-N-R-G-F-F-D-Y-KK-E-V
45 cpx. FR. 04. 04FR AUK	NI	R	IV-AI-I-Q-TP-EG-Q	G	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
46 BF. BR. 07. 07BR FPS625	N	R	IV-I-I-TP-I-EG-V-Q	G	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
47 BF. ES. 08. P1942	IV	QI	I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
48 01B. MY. 07. 07MYKT021	SS	R	IV-EI-I-Q-RATP-TAPA-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
49 cpx. GM. 03. N26677	N	IV	QI-I-Q-TP-EG-V-Q	A	L	V-NHPS-E-T-H-D-R-F-G-F-GF-D-Y-KK-E-V
50 A1D. GB. 10. 12792	A	C	PV-KI-E-G-P	R	L	DN-D-H-D-R-F-G-F-GF-D-Y-KK-E-V
51 01B. SG. 10. 10SG HM021	IV	QI	I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
52 01B. MY. 03. 03MYK1018 1	IV	QI	I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
53 01B. MY. 11. 11FIR164	GR	LG	TOI-TPAAAE-EVGA-EG-V-K	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
54 01B. MY. 09. 09MYSB023	S	IV	QI-I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
55 01B. CN. 10. HNC5102056	R	IV	QI-I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
56 cpx. FR. 10. 10FR patient A	IV	QI	I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
57 BC. CN. 09. 09YNLX1959	IV	QI	I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
58 01B. MY. 09. 09MYPR37	IV	QI	I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
59 01B. CN. 09. 09LNA423	KA	Q	IEQ-TP-VTEG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
60 BC. IT. 11. BAV499	C	V	S-I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
61 BC. CN. 10. J1100010	S	R	IV-DI-I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
62 BC. CN. 10. YNLF13	R	IV	QI-I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
63 02A1. RU. 10. 10RU6637	R	IV	QI-I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
64 BC. CN. 09. YNLF31	N	R	IV-EI-I-Q-TP-EG-V-Q	AR	L	DD-E-G-R-F-G-F-F-D-Y-KK-E-V
65 cpx. CN. 10. YNLF01	X	IV	QI-I-Q-TP-EG-V-Q	DR	L	DRTE-G-V-E-E-G-R-F-G-F-F-D-Y-KK-E-V
67 01B. CN. 11. ANHUI HF115	IV	QI	I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
68 01B. CN. 11. ANHUI WH73	N	IV	QI-I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
69 01B. JP. 05. 05JPMYC113SP420	N	IV	QI-I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
70 BFI. BR. 10. 10BR PE004	IV	QI	I-Q-TP-EG-V-Q	QR	L	IN-N-D-F-H-E-R-G-L-F-WK-E-V
71 BFI. BR. 10. 10BR PE008	IV	QI	I-Q-TP-EG-V-Q	QR	L	IN-N-D-F-H-E-R-G-L-F-WK-E-V
72 BFI. BR. 10. 10BR MG002	X	IV	QI-I-Q-TP-EG-V-Q	QR	L	IN-N-D-F-H-E-R-G-L-F-WK-E-V
73 06. DE. 01. 06D 91	IV	QI	I-Q-TP-EG-V-Q	A	L	V-NHPS-E-T-H-D-R-F-G-F-GF-D-Y-KK-E-V
74 01B. MY. 10. 10BRYP268	IV	QI	I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
78 cpx. CN. 13. YNLC19	IV	QI	I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
85 BC. CN. 14. 14CN SCYB2	S	R	IV-AI-I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
86 BC. CN. 13. 13YNHS18	S	R	IV-AI-I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
87 cpx. CN. 12. DH32	S	R	IV-AI-I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
88 BC. CN. 05. 05YNL255g	N	IV	QI-I-Q-TP-EG-V-Q	D	V	T-M-N-DSV-R-E-D-N-R-G-F-F-D-Y-KK-E-V
0. CM. 96. LA51YBF35	NA	K	FA-SD-N-Q-TSPD-PLPO-C-PG-V	E	ADR-G-P-Y-PON-L-F-S	HK-D-R-F-G-F-F-D-Y-KK-E-V
0. CM. 96. LA52YBF39	NALK	FA	A-PAPS-DDPE-C-PG-EL	E	AAR-GVP-Y-PON-L-F-S	HS-D-R-F-G-F-F-D-Y-KK-E-V
0. CM. 99. 99CMU4122	NALR	R	FP-SAI-K-TSP-EPE-C-XG-PV	E	AAR-G-P-Y-PON-L-F-S	HS-D-R-F-G-F-F-D-Y-KK-E-V
0. CM. x. pCM02 3	ENALR	R	FE-AI-K-TSP-EPE-C-QV	E	AAR-G-P-Y-PON-L-F-S	HS-D-R-F-G-F-F-D-Y-KK-E-V
0. ES. 01. Res105 HIV Group0	NALR	K	FE-AA-KTK-TSP-EPE-C-EG	P	ADR-G-P-Y-PON-L-F-S	HO-D-R-F-G-F-F-D-Y-KK-E-V
0. FR. 06. LA55RBF206	N	K	FA-TE-T-Q-TSPE-PEPE-C-PG-V	E	AAR-G-P-Y-PON-L-F-S	HO-D-R-F-G-F-F-D-Y-KK-E-V
0. GA. 11. 11GAb6352	NVLG	DK	FG-A-TR-TSP-ESE-P-AG-V	E	AIAEK-G-PN-Y-PON-E-L-F	DS-HO-D-R-F-G-F-F-D-Y-KK-E-V
0. SN. 99. 99SE MP1299	NVLG	DI	FK-SA-G-TSP-DPE-C-PG-QI	E	AAR-G-P-Y-PON-L-F-S	HO-D-R-F-G-F-F-D-Y-KK-E-V
0. SN. 99. 99SE MP1300	NVLG	DK	FK-SA-K-TSP-EPE-C-PG-QV	E	AAR-G-SN-H-PON-L-F-S	HO-D-R-F-G-F-F-D-Y-KK-E-V
0. US. 10. LTNP	NVLG	K	YD-AS-KTRTIRTRTSP-ESE-PG-V	E	AAR-G-PT-H-PON-L-F-S	HO-D-R-F-G-F-F-D-Y-KK-E-V
N. CM. 96. U14296	KI	IV	EI-Q-OTRE-TPVEP-AG-V-Q	A	TR-T-RDN-OTL	Y-EE-D-R-F-G-F-F-D-Y-KK-E-V
N. FR. 11. NI. FR 2011	KI	IV	EI-Q-OTPG-AAVEP-AG-V-Q	A	TR-T-RDN-OTL	Y-EE-D-R-F-G-F-F-D-Y-KK-E-V
P. CM. 06. U14788	NA	K	LVA-A-KIKO-TTPPTPD-PTTPTVP-EG-EI-K	E	AQGGK-P-KFSSKN-L-F	D-H-C-F-F-F-D-VY-PE-AE-V
P. FR. 09. RBF168	NA	K	LVA-A-NO-TATPT-ETP-SG-EI-K	E	AQGGK-P-KYNSKN-L-F	D-H-C-F-F-F-D-VY-PE-AE-V
CPZ. TZ. 06. TAN5	NL		FGK-GAOKAIOA-IH-TSNEP-Q-Q	Q	TR-PON-OTL-DEMTH	S-R-A-M-E-L-W-FW-PK-AA-T-M-N-V
CPZ. US. 85. US Marilyn	IV	E	N-L-Q-TOT-TA-EG-PV-Q	Q	TR-PON-OTL-DEMTH	S-R-A-M-E-L-W-FW-PK-AA-T-M-N-V
GOR. CM. 12. SIVgor_BID02	NA	K	LVA-A-D-Q-TSP-DPE-C-PG-IV	E	AQK-G-P-Y-PON-L-F	DS-HT-F-G-F-F-D-Y-KK-E-V
GOR. CM. 13. SIVgor_BPID15	NA	K	LVA-A-D-IHQ-TTPE-DIPG-PG-KT	E	AK-EK-P-KYNSKN-L-F	DS-HT-F-G-F-F-D-Y-KK-E-V

	HXB2 premature Nef end	normal Nef end	
B.FR.83.HXB2	PD-QNYTPGGVRYPLTFGWCYKLVPEPKIEE.ANKGENTSLHPVSLHGMD.D.PEREVLEWRFSRLAFHWHVARELHPEYF.K.....NC*		205
A1.CM.08.886.24	--W-----I-----F-----EEV.R.-TE--N--MCQ-----D--T-I-K--H--K-I--M--FY.....D--		205
A1.CY.08.CY236	--W-----I-----F-----D.-EV.K.ETE--N--ICO-----E.-E-T-R-E-----LK-R-Q-----FY.....D--		45
A1.KE.11.DEMA111KE002	--W-----I-----F-----D.-KEV-----E--NC--M-Q-IE-----E--V-K-----LR-R-----FY.....D--		205
A1.NG.10.10NG040248	--W-----I-----H-----F-----D.-EV.K.-TE--NC--M-Q-IE-----E--K-T-Q-K-S-----LR-R-----FY.....D--		215
A1.PK.14.DEMA114PK001	--W-----I-----F-----F-----D.-EEV.R.-E--N--MCO-----E-G-T-M-----LR-----FY.D-----		208
A1.RW.11.DEMA111RW002	--W-----I-----F-----F-----D.-EEV.K.-E--N--ICO-----E-T-K-K-----LK-L-----DFY.....D--		210
A1.UG.11.DEMA110UG009	--W-----I-----F-----F-----M.-EEV.K.-AE-DNC-INO-----D-T-V-----R-----FY.....D--		205
A1.ZA.04.503.15344.T10.A1	--WH-----T-----F-----N.-SEV-----TE--N--ICO-I-----K--K--H-LR-R-----YDFY.....D--		213
A2.CM.01.01CM.1445MV	--W-----I-----F-----D.-AENV-----TE--N--ICO-----E-E-K-R-K-----LR-L-Q-----FY.....D--		204
A3.SN.01.DD1579	--W-----T-----F-----DQASV-----TG-----CO-----K-K-M-----LK-T-M-----FY.....D--		207
A4.CD.97.97CD.KCC2	--W-----I-----F-----EAV-----TG--N--ICO-----M-K-----LK-R-K-----FY.....D--		204
A6.BY.13.PV85	--W-----I-----F-----D.-AENV-----TE--N--ICO-----E-E-K-R-K-----LR-L-Q-----FY.....D--		212
A6.CY.09.CY255	--W-----I-----F-----D.-ADV-----TE--N--ICO-----E-K-K-Q-----LT-R-M-----FY.....D--		46
A6.RU.11.11RU6950	--W-----E-----F-----D.-ADV-----TE--N--ICO-----E-K-K-Q-----LT-R-M-----FY.....D--		210
A6.UA.12.DEMA112UA014	--W-----T-----F-----D.-AENV-----TE--N--ICO-----E-K-M-K-----LK-I-Q-----FY.....D--		207
B.BR.10.10BR.RJ032	--W-----T-----F-----F-----QV-----IN--M-Q-----M-K-M-K-----K-----Y-DW-----Q#D		220
B.CA.07.502.1191.03	--W-----T-----F-----EQV-----TV-TNN-G-----E-K-V-K-----K-K-F-RDR-----D--		207
B.CH.08.M2.0803101.NFLG8	--W-----T-----C-----F-----D.-V-----T--IN--M-Q-----E-K-V-K-----M-----FY.....D--		214
B.CN.12.DEMB12CN006	--WH-----I-----F-----LD-EQV-K.-TE--NC--MNO-----K-V-----L-KD-Y-D-Y-G-----D--		206
B.CU.14.14CU005	--W-----I-----F-----E.V-----N--A-M-Q-----E-T-----G--N-----M-----K-----Y-----D--		99
B.DE.13.366396	--W-----K-----I-----C-----F-----EQV-Q.-E--IT--G--N-----M-----K-----Y-----D--		208
B.ES.14.ARP1195	--W-----K-----I-----C-----F-----DKE-----Q--NC--M-Q-----K-V-K-L-N-----Y-----D--		207
B.FR.11.DEMB11FR001	--W-----I-----F-----DKE-----Q--NC--M-Q-----K-V-K-L-N-----Y-----D--		224
B.HT.05.05HT.129389	--W-----E-----T-----F-----F-----D.-QV-K.D.E--IN--M-Q-----M-K-H-LQ-----K-----Y-----D--		126
B.JP.12.DEMB12JP001	--W-----T-----F-----F-----E.V-----TV--NC--MN-----G-V-K-----K-----Y-----D--		208
B.KR.07.HP.18.07JHS10.3909	--W-----T-----F-----F-----D.-EEV.R.-TV--NC--ANN-----M-----K-----Y-----D--		207
B.RU.11.11RU21n	--W-----T-----F-----D.-EEV.R.-TV--NC--ANN-----M-----K-----Y-----D--		207
B.SE.12.SEG00057	--W-----T-----W-----F-----E.-NSE-TN-A-E-----G-V-K-----M-----Y-----D--		217
B.TH.10.DEMB10TH002	--WH-----F-----C-----F-----A-EDV-K.VTE-RNC-MN-----M-K-K-----Q-----Y-----D--		205
B.US.16.2609	--W-----F-----F-----D.-REV-----TA-DNR-M-----E-ADG-Q-K-L-RR-----I-----Y-----D--		208
C.BR.11.DEMC11BR035	--WS-----F-----F-----D.-REV-----E--NC--CO-----E-EH-K-Q-IQ-HR-M-----FY.....D--		208
C.CN.10.YNFL19	--W-----T-----F-----F-----D.-REV-----E--NC--M-Q-----E-DD-Q-K-S-RR-L-----Y-----D--		213
C.DE.10.622166	--W-----T-----F-----F-----D.-REV-----E--NC--M-Q-----E-DD-Q-K-S-RR-L-----Y-----D--		203
C.ES.14.ARP1198	--W-----I-----F-----D.-EEV.K.-N-E-NC-I-----E-EHK-V-S-RR-----FX-----D--		209
C.ET.08.ET104	--W-----I-----F-----D.-REV-----TSQ-NC-C-----E-EY-Q-K-Q-HR-----R-----Y-----D--		208
C.IN.15.NIRT008	--W-----I-----F-----D.-REV-----E--NC--M-Q-----E-DH-K-K-Q-HK-M-----FY.....D--		208
C.MW.09.703010256.CH256.w96	--W-----I-----F-----D.-REV-----G--NC--L-QY-A-----DH-M-K-S-RR-M-----Y-----D--		209
C.NG.10.10NG082523	--W-----I-----F-----D.-REV-----E--DNC-M-Q-----E-EH-K-K-----RR-M-----Y-----D--		208
C.NP.11.11NP016	--W-----I-----F-----D.-REV-----E--DNC-M-Q-----E-EH-K-K-----RR-M-----Y-----D--		209
C.PK.14.DEMC14PK009	--W-----I-----F-----D.-REV-----E--DNC-M-Q-----E-EH-K-K-----RR-M-----Y-----D--		209
C.SE.13.SEG000311	--W-----I-----F-----D.-QIV-----E--NC--I-----E-ED-M-K-IQ-HK-M-----FY.....D--		208
C.TZ.08.707010457.CH457.w8	--W-----L-----F-----D.-KEV-----ETE--N--M-----E-EH-K-K-M-RR-M-----K-----Y-----D--		208
C.US.11.17T84.4G8	--W-----I-----F-----D.-SEV-----N-E--NC--M-Q-----E-ED-K-K-S-RR-M-----Y-----D--		218
C.ZA.13.DEMC13ZA152	--W-----I-----F-----D.-REV-----E--DNC-M-Q-----E-OYG-Q-K-L-RR-I-----Y-----D--		214
C.ZM.11.DEMC11ZM006	--W-----I-----F-----D.-QEA-----H-RDDSC-M-M-Q-IE-----EH-I-M-K-TQ-RR-L-----WY-----D--		206
D.BR.10.10BR.RJ108	--W-----I-----C-----FE-----D-QVVG-----TE--NC--ICO-AE-S-----V-N-----E-K-KY-----D--		96
D.CD.03.LA17Mu0o	--W-----T-----C-----FE-----D-RVV-G.ETE--C-----Q-----E-T-----V-K-N-----E-K-QK-----F-----D--		207
D.CM.10.DEMD10CM009	--W-----T-----C-----FE-----D-RVV-G.ETE--C-----Q-----E-T-----V-K-N-----E-K-QK-----F-----D--		211
D.CY.06.CY163	--W-----I-----F-----L-EEV-K.-TE--NC--M-Q-----Q-----I-N-N-----E-K-Q-----FY.....D--		45
D.KE.11.DEMD11KE003	--WH-----I-----FE-----L-EEV-K.-TE--NC--M-Q-----Q-----I-N-N-----E-K-Q-----FY.....D--		207
D.KR.04.04KR08	--WH-----I-----FE-----D.-KEV-----TE--SC-I-Q-----E-T-K-V-N-K-----E-K-S-----FY.....D--		203
D.TZ.01.288	--W-----I-----F-----D.-KEV-----DTE--NC--MCO-----E-Q-----K-N-----E-K-KI-----Y-----D--		208
D.UG.10.DEMD10UG004	--W-----I-----F-----D.-KEV-----DTE--NC--MCO-----E-Q-----K-N-----E-K-KI-----Y-----D--		207
D.UG.11.DEMD11UG003	--W-----I-----F-----D.-IDAKEA-----DTE--NC--ACO-----E-T-----M-N-----E-K-V-----DFY.....D--		208
D.YE.02.02YE516	--W-----I-----H-----FE-----D-KMV-----E-E-DKC-MHO-----G-----K-V-N-K-----E-K-KT-----F-----D--		205
F1.A0.06.A0.06.ANG32			96
F1.AR.02.ARE933			90
F1.BR.10.10BR.RJ015			104
F1.BR.11.DEMF11BR037	--W-----I-----L-----F-----D.-EDV-K.-E--NC--M-----E-EDK-V-K-----LR-I-R-D-Y-D-----D--		217
F1.CY.08.CY222	--W-----I-----L-----F-----D.-EEV-K.-E--NC--M-Q-----ADG-K-K-T-LR-I-RF-----Y-D-----D--		45
F1.ES.02.ES.X845.4	--W-----T-----L-----F-----D.-EEV-K.-E--NC--M-Q-----EDG-K-Q-----LK-I-R-----Y-OD-----D--		206
F1.ES.11.VA0053.nfl	--W-----T-----L-----F-----D.-EEV-K.-E--NC--M-Q-----EDG-K-Q-----LK-I-R-----Y-OD-----D--		216
F1.FR.04.LA221eRe	--W-----I-----F-----D.-EEV-K.-E--DNC--M-Q-----E-GD-Q-K-----R-K-K-----FY-ON-----D--		206
F1.R0.03.LA20duCl	--W-----L-----F-----D.-EEV-R.-E--C--M-Q-----EDG-R-K-----LR-L-K-----FY-D-----D--		207
F1.RU.08.D88.845	--W-----X-----F-----D.-EEV-K.-E--TNC-I-Q-IE-----ED-M-K-T-MR-I-K-K-----FY-D#-----D--		215
F2.CM.02.02CM.0016BBY	--W-----T-----F-----F-----D.-EEV-K.-E--TNC-I-Q-IE-----ED-M-K-T-MR-I-K-K-----FY-D#-----D--		132
F2.CM.10.DEMF210CM007	--W-----T-----L-----F-----S-EEV-K.-E--NC--M-----E-ENG-Q-K-S-RR-L-K-----FY-TE#-----D--		206
F2.CM.11.DEURF11CM026	--W-----T-----L-----F-----S-EEV-K.-E--NC--M-----E-ENG-Q-K-S-RR-L-K-----FY-TE#-----D--		211
G.CD.03.LA23L1Ed	--W-----T-----F-----F-----L-EE-----T--N--ICO-IE-----AD-V-S-RR-I-----DFY.....D--		211
G.CM.08.709.10	--W-----T-----F-----F-----D.-AE-----N--ICO-----E-EH-R-K-S-RR-L-----K-----FY.....D--		206
G.CM.10.DEMG10CM008	--W-----T-----F-----F-----MD-AE-----T--NC--ICO-----E-ED-V-S-RR-I-----K-----FY.....D--		213
G.CM.10.DEURF10CM020	--W-----I-----F-----D.-ADV-----I-R--N--I-Q-----E-GDN-V-K-S-RR-----I-----Y-----D--		208
G.CN.08.GX.2084.08	--W-----T-----F-----F-----MD-AEV-----E--N--ICO-Q-----E-ED-V-S-RR-R-----FY.....D--		208
G.ES.14.ARP1201	--W-----K-----I-----F-----D.-AEV-----N-E--N--ICO-IE-----E-ED-V-S-RR-I-----DFY.....D--		215
G.GH.03.03GH175G	--W-----T-----L-----F-----D.-AEV-----N-E--N--ICO-IE-----E-ED-V-S-RR-I-----DFY.....D--		208
G.GW.08.LAS71mNe	--W-----I-----F-----F-----E-M-AEV-----TN-----ICO-----E-ADK-V-S-RR-----DFY.....D--		207
G.KE.09.DEMG09KE001	--W-----I-----F-----D.-AE-----TR-RNT-ICO-----E-SD-K-K-S-RR-I-----Y-----Y-----D--		219
G.NG.12.12NG060409	--W-----T-----F-----F-----LD-AE-----TE--N--ICO-V-----DDK-V-S-RR-I-----DFY.....D--		211
H.CD.04.LA19KoSa	--W-----E-----F-----F-----D.-QDV-K.-E--NC--ICO-----E-M-K-S-RR-I-----T-QFY-----D*		205
H.CF.02.LA25LeM1	--W-----E-----F-----F-----D.-QEV-K.-E--TNC-ICO-----E-E-K-----I-K-----T-T-R-----FY.....D--		208
H.GB.00.00GBAC4001	--WH-----I-----C-----F-----D.-QEV-K.-E--N--MCO-----E-E-K-V-----H-R-R-----O-----FY.....D--		208
J.CD.03.LA26D1An	--W-----I-----F-----D.-REV-K.-E--DNC-ICO-----E-E-G-M-K-S-RR-I-----K-----Y-----D--		209
J.CD.07.J.97DC.KTB147	--W-----I-----F-----D.-REV-R.-E--DNC-ICO-----E-E-G-M-K-S-RR-I-----K-----Y-----D--		202
J.SE.93.SEG280.7887	--W-----I-----F-----D.-SEV-----TE--NC--M-Q-----E-ED-Q-K-S-RR-I-----FY.....D--		204
K.CD.97.97ZR.E0T811	--W-----I-----F-----D.-REV-----TE--NC--NO-E-EH-K-K-S-RK-----M-----Y-----D--		207
K.CM.96.96CM.MP535	--W-----I-----F-----D.-REV-----TTE-DNC-INO-----E-EH-I-M-K-S-RR-----D-----Y-----D--		216
01.AE.AF.07.569M	--W-----T-----F-----C-----F-----D.-STV-----D--NC--M-Q-IE-----E-I-K-A-RK-I-----Y-----D--		225
01.AE.CM.11.1156.26	--W-----I-----C-----F-----D.-REV-----D--NC--M-Q-IE-----E-ED-M-K-S-RR-I-----RY-----Y-D-----D--		204
01.AE.CN.12.DE0012CN011	--WH-----I-----C-----F-----D.-REV-----D--SC-INO-IE-----E-M-K-A-RK-I-----R-----Y-----D--		207
01.AE.HK.04.HK001	--W-----I-----C-----F-----D.-REV-----D--NC--M-Q-IE-----E-ED-M-K-A-RK-I-----FY.....D--		207
01.AE.IR.10.10IR.THR48F	--W-----I-----C-----F-----DREV-----D--NC--M-Q-IE-----E-ED-M-K-A-RK-I-----FY.....D--		205
01.AE.JP.11.DE0011JP003	--W-----I-----C-----F-----DREV-----D--NC--M-Q-IE-----E-ED-M-K-A-RK-I-----FY.....D--		206
01.AE.SE.11.SEG01018	--WH-----I-----C-----F-----D.-Q-----N--NC--M-Q-AE-----E-I-K-S-RK-I-----R-FY-RD-----D--		206
01.AE.TH.10.DE0010TH001	--WH-----I-----C-----F-----I-ID-REV-----N--NC--M-Q-IE-----E-M-K-A-RK-I-----I-----Y-----D--		200
01.AE.TH.90.CM240	--W-----I-----F-----C-----F-----DREV-----D--NC--M-Q-IE-----E-M-K-A-RK-I-----I-----Y-----D--		205
01.AE.US.05.306163.FL	--W-----T-----F-----C-----F-----D.-REV-----D--NC--L-Q-IE-----E-M-K-A-RK-----D-----Y-----D--		198
02.AG.CM.10.DE0010CM013	--W-----T-----F-----F-----LD-VE-----R-----N--T-K-----K-----FY-D-----D--		216
02.AG.DE.10.701114	--W-----I-----F-----F-----MD-ADV-----H--N--ICO-----E-DHG-V-RS-SK-I-----K-----FY-DX-----D--		211
02.AG.GW.05.CC.0048	--W-----I-----F-----F-----MD-TEV-----L-E--N--Q-----E-ED-V-X-X-----X-----D--		192

